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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file pto_PLACENTA.txt, created 24
25 January 2001, having 26,548,337 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches — and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species — there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25 Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,
30 particularly those with polygenic etiology.

Summary of the Invention

35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
25 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof 35 wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
10 placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
15 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

20

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

10 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution
15 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the
20 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
25 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
30 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
35 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by
10 microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the
20 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

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FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly

include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR
(nonredundant) divisions. GenBank is produced by the
National Institutes of Health and is maintained by the
5 National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
eukaryotic organisms will also prove useful as genomic
10 sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
15 the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
20 mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into
25 process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
given genomic region. In such case, the input often will
30 be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
experimental confirmation is identified. Experimental
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query
5 criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable
10 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,
15 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual
25 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
30 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the
10 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with
15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer
25 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify
30 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it
5 has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
15 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
20 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
25 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
30 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
35 about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the
10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual,
15 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,
25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes
30 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single
35 exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
35 libraries targeted at a particular biological question,

R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
5 expression only of those genes found in EST libraries,
shown herein to represent only a fraction of expressed
genes. Furthermore, such libraries - and thus microarrays
based thereupon - are biased by the tissue or cell type of
message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message
successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the
methods of the present invention enable sequences that do
not appear in EST or other expression databases to be
15 determined - subsequently arrayed for expression
measurements could not, therefore, have been represented as
probes on an EST microarray. And as further demonstrated
in the examples, *infra*, the remaining population of genes
identified from genomic sequence by the methods of the
20 present invention - that is, the one third of sequences
that had previously been accessioned in EST or other
expression databases - are biased toward genes with higher
expression levels.

Representation of a message in an EST and/or cDNA
25 library depends upon the successful reverse transcription,
optionally but typically with subsequent successful
cloning, of the message. This introduces substantial bias
into the population of probes available for arraying in EST
microarrays.

30 In contrast, neither reverse transcription nor
cloning is required to produce the probes arrayed on the
genome-derived single exon microarrays of the present
invention. And although the ultimate deposition of a probe
on the genome-derived single exon microarray of the present
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-
20 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the
30 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-
30 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
20 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

- 5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

- 10 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

- Alternatively, or in addition, the color, hue, 15 density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be 20 indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

- As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, 30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

- Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show
5 predictions of a plurality of different functions.
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes
5 and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis,
10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought
15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease,
20 neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

25 A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all
30 such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may
35 be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of
5 expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in
10 other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which
15 are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was
20 measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten
25 tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have
30 significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon
35 microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
5 46(3):425-8 (1999)), in drug discovery screens (see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
10 Expression Profile Analysis of Human Breast Cancer
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
15 appreciated that even those probes that show no change in
expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
20 failure of the agent to change a gene's expression level is
evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
25 lead compound discovery or in subsequent screening of lead
compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

30 WO 99/58720 provides methods for quantifying the
relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);

5 Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase
35 hybridization, however — that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human *cot1* DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, inter alia, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, inter alia, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

30 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

35 All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
15 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
35 gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
15 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
30 sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays
5 prepared according to Example 1 were hybridized in a series
of simultaneous two-color fluorescence experiments to (1)
Cy3-labeled cDNA synthesized from message drawn
individually from each of brain, heart, liver, fetal liver,
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100
10 cells, and (2) Cy5-labeled cDNA prepared from message
pooled from all ten tissues and cell types, as a control in
each of the measurements. Hybridization and scanning were
carried out using standard protocols and Molecular Dynamics
equipment.

15 Briefly, mRNA samples were bought from commercial
sources (Clontech, Palo Alto, CA and Amersham Pharmacia
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were
incorporated during separate reverse transcriptions of 1 µg
of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
20 and 2 µg random 9mer primers as follows. After heating to
70°C, the RNA:primer mixture was snap cooled on ice. After
snap cooling on ice, added to the RNA to the stated final
concentration was: 1X Superscript II buffer, 0.01 M DTT,
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
30 column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; 5 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose 10 expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 15 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 25 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 35 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in
30 the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
35 chromosome RNA-binding motif (Chai et al., *Genomics*

49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.

The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
35 sequences. These are set out as PEPTIDE SEQ ID NOS.: The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
30 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously
35 been shown to be expressed — the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	5				
912	14087	27162	8.68				
1070	14230		3.01				
1330	14487	27555	10.9				
1645	14707	27882	1.82				
1669	14818	27901	4.94				
1784	14913	28008	1.03				
1788	14937	28030	1.67				
1794	14943	28036	8.53				
1939	15082	28163	1.57				
2034	15175	28285	2.68				
2234	15368	28497	3.39				
2353	15484	28616	2.53				
3256	16429	29447	3.75				
3637	16702	29713	1.48				
3604	16768	29763	10.5				
3651	16814		0.84				
3747	16908	29812	0.68				
4057	17213		0.94				
4314	17457	30445	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4390	17539	30520	0.87				
4457	17597		1.69				
4512	17651	30639	0.61				
4659	18088	31064	1.86				
5002	18131		0.6				
5157	18279	31244	5.14				
5169	18280	31255	1.24				
5371	18574	31442	1.76				
5371	18574	31443	1.78				
5539	18735		4.12				
5714	18907		7.26				
5706	18735		3.31				

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5858	18048	32354	4.22				
6146	28820	32868	1.61				
6174	18350	32866	1.92				
6546	19708		1.01				
6679	18338	33226	1.25				
6679	18338	33227	1.25				
7275	20358	33812	1.42				
7276	20358	33813	1.42				
7569	20841	34117	1.18				
7569	20841	34118	1.18				
8251	21333	34851	1.44				
8682	21762	35206	1.14				
9061	22140	36884	0.76				
9061	22140	36885	0.76				
9734	22789	39373	3.82				
9888	23007	39802	0.56				
10086	23124	38725	1.51				
10229	23264	39853	0.88				
10843	23677	37286	0.74				
10843	23677	37287	0.74				
10822	24005		2.32				
11280	24346		1.76				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23835	37581	1.36				
11749	23835	37582	1.36				
11782	24782		2.09				
12057	25038	38746	1.56				
12823	25419		2.08				
12867	25828	31880	1.5				
8177	19353	32700	10.82	9.8E+00	AJ238028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8195	21277	34800	1.5	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9844	22883	36575	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9844	22883	36576	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.0E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.0E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10538	23670	37279	0.93	9.0E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIf1 polypeptide 2 (Gtf2h2) genes, complete cds
10538	23670	37280	0.93	9.0E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIf1 polypeptide 2 (Gtf2h2) genes, complete cds
2731	19949	28959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polypeptide mRNA, partial cds
2731	19949	28960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polypeptide mRNA, partial cds
2890	16188	29182	3.08	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130900.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
7625	20695	34171	0.6	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31586	2.59	9.1E+00	AF095608.1	NT	Leuiscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095608.1	NT	Leuiscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9630	22685		1	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6160	19336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3934592 3'
6510	19675	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
6510	19675	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
453	13649	26685	1.79	8.4E+00	6031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9654	21097	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (seal2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21428		0.98	7.9E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7501	20578		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8566	21637	35174	1.42	7.6E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8558	21637	35175	1.42	7.5E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5621	16108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	602126870F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285508 5'
8953	22032	35573	3	7.4E+00	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35574	3	7.4E+00	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3042	16218	28238	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	28239	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33760	1.07	7.2E+00	BE170030.1	EST_HUMAN	LOC10813-200300-031-007 H10613 Homo sapiens cDNA
7289	20381	33636	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7289	20381	33639	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9798	22838		8.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11688	24745	38437	2.44	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10187	23224	36818	2.76	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)
11628	24584	38261	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS3
8478	21559	35083	3.17	6.9E+00	P35879	SWISSPROT	80S RIBOSOMAL PROTEIN L4 (L2)
10559	23594	37200	1.12	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10679	28814	37219	0.8	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
8092	21174	34688	1.64	6.8E+00	W03412.1	EST_HUMAN	2807c11.1 Scores melanocyte 2NIH-H1 Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34689	1.64	6.8E+00	W03412.1	EST_HUMAN	2807c11.1 Scores melanocyte 2NIH-H1 Homo sapiens cDNA clone IMAGE:291860 5'
8333	22409		1.62	6.8E+00	P38307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10413	23448	37053	3.6	6.8E+00	Q09570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
8398	18500		0.85	6.8E+00	Q08028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6675	19834	33223	0.88	6.8E+00	BF672121.1	EST_HUMAN	802162573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
8234	20228		0.55	6.8E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.8E+00	Q07E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.8E+00	Q07E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23878	37498	0.47	6.8E+00	H28330.1	EST_HUMAN	Yn80066.c1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.8E+00	Q10308	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52 COAT PROTEIN GP36]
10512	23547	37158	0.52	6.5E+00	BE868001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680989 5'
8943	22882	36574	1.34	6.2E+00	AY010801.1	NT	Schizosaccharomyces pombe unknown mRNA
10787	23620	37444	0.7	6.2E+00	6754821	NT	Mus musculus marmosin class 2, alpha B1 (Mar2b1), mRNA
7181	20313	33766	1.8	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36855	0.49	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genome DNA, 1168001-1485000 nt, position (87)
10732	23785	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23785	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19809	33197	7.14	6.9E+00	AF158142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk46) genes, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11833	24819		3.02	5.9E+00	BE98630.1	EST_HUMAN	601646279F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830461 5'
3613	16777		1.15	5.8E+00	7681557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20304	33855	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20384	33856	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20803		1.34	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLG-TYPE (POLIII)
11289	24355	37898	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysoczyme C, complete cds
11289	24355	37897	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysoczyme C, complete cds
11765	23851	37881	2.62	5.6E+00	Q56278	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32908	0.74	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRC4
8882	23021		0.68	5.6E+00	P19883	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24087		1.48	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.6E+00	P11930	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33636	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7069	20122	33637	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559		1.04	5.4E+00	Q89435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.62	5.4E+00	Q81062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1G;
8054	21137		1.62	5.4E+00	Q81062	SWISSPROT	LIPOVITELLIN LV-2]
8969	22078	35818	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8969	22078	35819	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10242	23277	36870	1.45	5.4E+00	Q17084	SWISSPROT	RHODOPSIN
10242	23277	36871	1.45	5.4E+00	Q17084	SWISSPROT	RHODOPSIN
4908	18038	31024	1.47	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CBH-20
8270	21952		3.39	5.3E+00	P64098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9184	22882		0.72	5.3E+00	AB034930.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11828	24814	38816	1.51	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5590	18775		1.18	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0891-270400-186-009 HT0891 Homo sapiens cDNA
10583	23618		0.98	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposible element reverse transcriptase gene, partial cds
11470	24629		1.83	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
9182	22240	35784	0.94	5.1E+00	Q16905	SWISSPROT	RHODOPSIN
10030	23068	36687	1.33	5.1E+00	P08182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6415	19584	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE-4124114 5'
10397	23432		0.7	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE-4131509 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10645	23678	37288	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24624	38304	7.24	5.0E+00	Z83890.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10437	23472		0.70	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		12.39	4.8E+00	AF185253.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8348	21429	34953	0.6	4.8E+00	BF367809.1	EST_HUMAN	RC3-GN0042-100800-011-010 GN0042 Homo sapiens cDNA
8736	21817		4.92	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240652.1	EST_HUMAN	601875884F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088718 5'
301	13517	26550	1.85	4.7E+00	BF240652.1	EST_HUMAN	601875884F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088718 5'
3347	16520	28534	1.02	4.7E+00	AL103280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7862	21012	34522	0.69	4.6E+00	U97698.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9397	22471	36036	1.1	4.6E+00	BE846437.1	EST_HUMAN	768810.1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3202098 3' similar to TR-O75140 O75140 KIAA0845 PROTEIN; contains element PTR5 repetitive element
9397	22471	36037	1.1	4.6E+00	BE846437.1	EST_HUMAN	768810.1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3202098 3' similar to TR-O75140 O75140 KIAA0845 PROTEIN; contains element PTR5 repetitive element
10600	23635		0.63	4.6E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
7847	20997		0.7	4.5E+00	AF126177.1	NT	Issachentia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11904	24892	38593	1.87	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12038	25039	38747	1.53	4.5E+00	BF688941.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280218 5'
3105	16281	28296	0.84	4.4E+00	BF530853.1	EST_HUMAN	602072595F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4216284 5'
3105	16281	28297	0.84	4.4E+00	BF530853.1	EST_HUMAN	602072595F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4216284 5'
6331	16302		1.58	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (Ia) associated invariant chain
6245	19419		0.77	4.3E+00	AF056879.1	NT	Homo sapiens neutrophil collagenase (GLGNA) gene, promoter region and 5'UTR
7596	20668	34142	2.53	4.3E+00	Y13402.1	NT	Plasmodium falciparum R238-var1 gene, exon 1
7792	20948	34341	0.98	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11101	24174	37809	14.74	4.3E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5694	18928		4.1	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5711	18904	32189	1.07	4.2E+00	P61826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5880	19070		0.71	4.2E+00	O27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
6911	20228	33657	1.97	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6811	20228	33656	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22238	35783	5.3	4.2E+00	A809013.1	EST_HUMAN	wf67g03.x1 Source_NFL_T_GBC_S4 Homo sapiens cDNA clone IMAGE:2360682 3'
10122	23160	38750	1.03	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWININ PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-18) (DOCT1)
10352	23387		0.47	4.2E+00	P40888	SWISSPROT	HEXOSE TRANSPORTER HXT8
7261	20344	33798	0.98	4.1E+00	BE263668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351634 5'
7839	20304	34396	7.66	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7860	21010		0.64	4.1E+00	AB041623.1	NT	Pan troponin yescerels mRNA for calcineurin A, complete cds
7863	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7863	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57503.1	NT	Pan troponin yescerels novel repetitive solo LTR element in the RN12 locus
9740	22805	36381	0.61	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22813	36498	2.25	4.1E+00	BF692425.1	EST_HUMAN	602247839F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:339208 5'
10370	23406		0.55	4.1E+00	AL235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 444
10514	23549		0.52	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
11124	24186		2.15	4.1E+00	P08718	SWISSPROT	(P27KIP1)
11214	24283		12.26	4.1E+00	BE885880.1	EST_HUMAN	HYPOTHETICAL PROTEIN HMLF1
3635	16789		0.72	4.0E+00	P38228	SWISSPROT	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
5575	20130	33546	0.93	4.0E+00	O62863	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5575	20130	33547	0.93	4.0E+00	O62863	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33546	0.98	4.0E+00	O62863	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33547	0.99	4.0E+00	O62863	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22153	36697	0.49	4.0E+00	Q14167	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10368	23403	37014	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23489	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23489	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37577	1.69	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.98	4.0E+00	P07664	SWISSPROT	GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS2C, NS2D, NS2E, NS2F, NS2G, NS2H, NS2I, NS2J, NS2K, NS2L, NS2M, NS2N, NS2O, NS2P, NS2Q, NS2R, NS2S, NS2T, NS2U, NS2V, NS2W, NS2X, NS2Y, NS2Z, NS3, NS3A, NS3B, NS3C, NS3D, NS3E, NS3F, NS3G, NS3H, NS3I, NS3J, NS3K, NS3L, NS3M, NS3N, NS3O, NS3P, NS3Q, NS3R, NS3S, NS3T, NS3U, NS3V, NS3W, NS3X, NS3Y, NS3Z, NS4, NS4A, NS4B, NS4C, NS4D, NS4E, NS4F, NS4G, NS4H, NS4I, NS4J, NS4K, NS4L, NS4M, NS4N, NS4O, NS4P, NS4Q, NS4R, NS4S, NS4T, NS4U, NS4V, NS4W, NS4X, NS4Y, NS4Z, NS5, NS5A, NS5B, NS5C, NS5D, NS5E, NS5F, NS5G, NS5H, NS5I, NS5J, NS5K, NS5L, NS5M, NS5N, NS5O, NS5P, NS5Q, NS5R, NS5S, NS5T, NS5U, NS5V, NS5W, NS5X, NS5Y, NS5Z, NS6, NS6A, NS6B, NS6C, NS6D, NS6E, NS6F, NS6G, NS6H, NS6I, NS6J, NS6K, NS6L, NS6M, NS6N, NS6O, NS6P, NS6Q, NS6R, NS6S, NS6T, NS6U, NS6V, NS6W, NS6X, NS6Y, NS6Z, NS7, NS7A, NS7B, NS7C, NS7D, NS7E, NS7F, NS7G, NS7H, NS7I, NS7J, NS7K, NS7L, NS7M, NS7N, NS7O, NS7P, NS7Q, NS7R, NS7S, NS7T, NS7U, NS7V, NS7W, NS7X, NS7Y, NS7Z, NS8, NS8A, NS8B, NS8C, NS8D, NS8E, NS8F, NS8G, NS8H, NS8I, NS8J, NS8K, NS8L, NS8M, NS8N, NS8O, NS8P, NS8Q, NS8R, NS8S, NS8T, NS8U, NS8V, NS8W, NS8X, NS8Y, NS8Z, NS9, NS9A, NS9B, NS9C, NS9D, NS9E, NS9F, NS9G, NS9H, NS9I, NS9J, NS9K, NS9L, NS9M, NS9N, NS9O, NS9P, NS9Q, NS9R, NS9S, NS9T, NS9U, NS9V, NS9W, NS9X, NS9Y, NS9Z, NS10, NS10A, NS10B, NS10C, NS10D, NS10E, NS10F, NS10G, NS10H, NS10I, NS10J, NS10K, NS10L, NS10M, NS10N, NS10O, NS10P, NS10Q, NS10R, NS10S, NS10T, NS10U, NS10V, NS10W, NS10X, NS10Y, NS10Z, NS11, NS11A, NS11B, NS11C, NS11D, NS11E, NS11F, NS11G, NS11H, NS11I, NS11J, NS11K, NS11L, NS11M, NS11N, NS11O, NS11P, NS11Q, NS11R, NS11S, NS11T, NS11U, NS11V, NS11W, NS11X, NS11Y, NS11Z, NS12, NS12A, NS12B, NS12C, NS12D, NS12E, NS12F, NS12G, NS12H, NS12I, NS12J, NS12K, NS12L, NS12M, NS12N, NS12O, NS12P, NS12Q, NS12R, 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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.98	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
12133	25113	38817	1.34	4.0E+00	P35611	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3891	16755	28770	5	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4441	17681		0.87	3.9E+00	A7055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5775	18957	32270	2.92	3.9E+00	BE514357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5775	18957	32271	2.92	3.9E+00	BE514357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6772	19327	33322	0.93	3.9E+00	AF288209.1	NT	Dicotyledonum discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19362	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
7619	20502	34068	4.26	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DP-4-beta-1) gene, exon 2
8812	21593	35128	2.44	3.9E+00	X65865.1	NT	Xlaenla mRNA for M4 muscarinic receptor
11674	23602	37624	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2693	15813		1.53	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6620	19685	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8627	21707	35244	1.12	3.8E+00	D44726.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9909	23037		0.6	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7804
12120	25100		11.66	3.8E+00	8631284	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4129	17282	30277	12.79	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8878	22454	38017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-39, and complete cds
11715	24755	39450	2.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	39451	2.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4277748 5'
12280	25198		1.87	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
609	19795	28814	3.78	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBJE10 5'
6369	18572	31440	0.76	3.6E+00	BF316316.1	EST_HUMAN	601801866F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4191018 5'
8749	21828	35364	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0001T808 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8749	21828	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0001T808 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8847	21828	35464	3.87	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8847	21928	35485	3.67	3.6E+00	AE004447.1	NT	<i>Pseudomonas aeruginosa</i> PA01, section 8 of 529 of the complete genome
9884	22804	38488	0.51	3.6E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9884	22804	38489	0.51	3.6E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11063	24167		3.21	3.6E+00	M80785.1	NT	<i>Escherichia coli</i> glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3319	16492	28508	1.04	3.5E+00	AF221538.1	NT	<i>Cryptosporidium felis</i> heat shock protein 70 (HSP70) gene, partial cds
6123	18302		1	3.6E+00	L42888.1	NT	<i>Borrelia burgdorferi</i> (strain 26016) outer surface protein (ospC) gene, partial cds
8341	18511	32868	0.93	3.5E+00	R19745.1	EST_HUMAN	hg40cd8.1 Scanes Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
8681	21781		0.58	3.6E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35851	0.99	3.5E+00	AA190698.1	EST_HUMAN	zp88b04.s1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9232	22310	35852	0.99	3.5E+00	AA190698.1	EST_HUMAN	contains Alu repetitive element; contains element MSR1 repetitive element;
9894	22743	36313	1	3.6E+00	AL161563.2	NT	<i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 53
10739	23772	37383	0.58	3.6E+00	AJ133723.1	NT	<i>Bos taurus</i> mRNA for Ran-binding protein 2, partial
1542	14694	27778	3.81	3.4E+00	AF254577.1	NT	<i>Brassica napus</i> RPB5d mRNA, complete cds
2644	16787	28882	1.07	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7518	20591	34065	2.33	3.4E+00	P04062	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7880	20832	34437	0.76	3.4E+00	P04062	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9876	21855		0.77	3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROMK1, ROMK2, ROMK3, ROMK4, ROMK5, and ROMK6 (KCNJ1) gene, complete cds
9274	22350	35901	0.77	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9312	22388	35939	0.54	3.4E+00	AJ250587.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 8
10471	23508	37119	3.35	3.4E+00	AF013167.1	NT	<i>Saccharomyces cerevisiae</i> MSS1 gene, complete cds
11822	24811	38508	2.06	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6183	18369	32719	0.97	3.3E+00	Q08689	SWISSPROT	POTASSIUM ION ALCOHOL DEHYDROGENASE
6183	18369	32720	0.97	3.3E+00	Q08689	SWISSPROT	POTASSIUM ION ALCOHOL DEHYDROGENASE
8077	21169	34678	1.03	3.3E+00	AF111168.2	NT	Homo sapiens estrone palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10681	23715	37321	1.04	3.3E+00	AP001511.1	NT	<i>Bacillus halodurans</i> genomic DNA, section 6/14
10681	23715	37322	1.04	3.3E+00	AP001511.1	NT	<i>Bacillus halodurans</i> genomic DNA, section 5/14
513	13707	28735	1.79	3.2E+00	X68422.1	NT	D. rerio zp-50 POU gene

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4193	13707	26735	0.78	3.2E+00	X88422.1	NT	D.refio zp-50 POU gene
4850	17688	30971	0.96	3.2E+00	4602404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5085	18880	32170	1.16	3.2E+00	P54824	SWISSPROT	SQUALENE-HOPENE CYCLASE
5086	18880	32171	1.16	3.2E+00	P54824	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18812	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18812	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19303	32968	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19303	32967	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.88	3.2E+00	P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7852	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
7852	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
8230	22308		6.28	3.2E+00	P13061	SWISSPROT	PERILIPIN [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
8730	22795	36388	1.31	3.2E+00	M86383.1	NT	S. cerevisiae trehalase (LVI) gene, complete cds
10345	23330	36981	2.06	3.2E+00	AB018081.2	NT	Oryzias latipes OIG88 gene for guanylyl cyclase C, complete cds
12219	25189		2.99	3.2E+00	L39336.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5895	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C25E2.02 IN CHROMOSOME I
7547	20619	34095	0.91	3.1E+00	P62178	SWISSPROT	TRIOSE PHOSPHATE PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (GTPT)
7804	20658		1.09	3.1E+00	AF303225.1	NT	Bacillus albacapsulatus peptidase (pae) gene, complete cds
8279	21381	34890	0.51	3.1E+00	P40885	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (8D1)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (8D1)
						SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9459	22676		3.7	3.1E+00	Q14957	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9528	22591	36102	0.55	3.1E+00	Q01148	SWISSPROT	Chlorella vulgaris chloroplast, complete genome
10100	23138	36738	0.78	3.1E+00	7524769	NT	HYPOTHETICAL 56.3 KD PROTEIN F203.5 IN CHROMOSOME III
10183	23230		0.56	3.1E+00	Q10125	SWISSPROT	DEOXYHYALURONIC SYNTHASE (DHS)
10543	23578	37187	4.09	3.1E+00	P48365	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN [ENVELOPE PROTEIN M]; MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
							retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt]
11751	25837		2.45	3.1E+00	P33515	SWISSPROT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds
11771	24783		2.49	3.1E+00	S66800.1	NT	
13019	25570		1.17	3.1E+00	U77888.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2889	18078	29095	0.95	3.0E+00	8923894	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
6464	18654	31693	1.29	3.0E+00	X59098.1	NT	S. aureus genes encoding S aureus DNA methyltransferase and S aureus restriction endonuclease
6686	18644	33234	0.82	3.0E+00	X59037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6688	18644	33235	0.82	3.0E+00	X59037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20388		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (SCH61)
7346	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8108	22187		1.62	3.0E+00	X67638.1	NT	B. napus DNA for myosinase
10501	23636	37146	0.66	3.0E+00	Q58905	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11250	24928	37067	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GCF)
11250	24328	37068	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GCF)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	16208	28324	2.69	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 63 of 64 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z38878.1	NT	F. principle gdcSPA gene for P-protein of the glycine cleavage system
7360	20439	33888	4.68	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33900	4.68	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20884	34160	6.19	2.9E+00	P46689	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8062	21135	34655	0.57	2.9E+00	P05944	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8062	21135	34656	0.57	2.9E+00	P05944	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34692	0.81	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3
9438	22512		0.82	2.9E+00	AL002153.2	NT	802017415F1 NC1 CGAP_Br64 Homo sapiens cDNA clone IMAGE:4153059 5'
1486	14639	27722	4.77	2.8E+00	AF186336.1	NT	Sequitus oedipus gene for seminal vesicle secreted protein semenogelin I
1682	14814		3.14	2.8E+00	AL101652.2	NT	Bufo marinus matriose K (matK) gene, partial cds; chloroplast gene for chloroplast product
7400	20535	34010	5.05	2.8E+00	6369724	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9813	22653		0.6	2.8E+00	BE595182.1	EST_HUMAN	Mus musculus endonuclease (LOC53423), mRNA
10628	20535	34010	1.53	2.8E+00	8369724	NT	Mus musculus endonuclease (LOC53423), mRNA
240	13462	28480	13.96	2.7E+00	6670306	NT	Mus musculus per-hexamer repeat gene 3 (Phw3), mRNA
240	13462	28481	13.96	2.7E+00	6670306	NT	Mus musculus per-hexamer repeat gene 3 (Phw3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5669	18963	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS5) gene including complete 5'UTR and complete cds
8168	22246		2.16	2.7E+00	AL116460.1	NT	Beiyue chinese strain T4 cDNA library under conditions of nitrogen deprivation
9632	21075	34587	0.91	2.7E+00	AW068191.1	EST_HUMAN	xc88e12x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17753
10718	23751		1.94	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4768	17831	30817	5.51	2.8E+00	AF068749.1	NT	CMC-BT0281-031193-087-NC4 B10281 Homo sapiens cDNA
5665	18959	32143	2.04	2.8E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5665	18959	32144	2.04	2.8E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Soc13), mRNA
5947	18133		2.85	2.8E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Soc13), mRNA
7727	26220		1.16	2.8E+00	AJ224638.1	NT	Mycobacterium fortuitum furA II gene
7878	20631		11.26	2.8E+00	AF236602.1	NT	Homo sapiens Surf-6 and Surf-6 genes
8249	21331	34847	1.17	2.8E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8249	21331	34848	1.17	2.8E+00	AJ132180.1	NT	(faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-63
9698	22898	36481	2.86	2.8E+00	AL161540.2	NT	(faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-63
10563	23598		1.91	2.8E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11281	24347	37884	2.2	2.8E+00	AF143676.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpas3), mRNA
12917	26064		3.3	2.8E+00	11418220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1492	14845	27726	3.03	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14845	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6986	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6986	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6986	20020	33426	0.77	2.5E+00	D30082.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxin, complete cds
7936	20366	34494	1.19	2.5E+00	AW948168.1	EST_HUMAN	QV4-F70005-110500-205-g07 FT0006 Homo sapiens cDNA
7885	21034	34547	0.82	2.5E+00	4502902	NT	Homo sapiens cldftrn, heavy polypeptide-like 1 (CLTCL1) mRNA
8304	22394	36631	1.66	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23066	36697	0.71	2.5E+00	BE287759.1	EST_HUMAN	801175778F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631060 5'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
12216	25167		1.85	2.5E+00	AF236665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3078	16254	28276	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5027	18156	31134	4.93	2.4E+00	4803352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	10813	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7638	20811	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120850F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20811	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120850F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406	21487		2.8	2.4E+00	AE001488.1	NT	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
8852	21831		1.72	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031288-011-005 PT0004 Homo sapiens cDNA
9028	22107	35648	8.89	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36954	2.31	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P06099	SWISSPROT	XYLULOSE KINASE (XYLULOSE KINASE)
10529	23569	37166	1.64	2.4E+00	BE326702.1	EST_HUMAN	h63306.x1 NC1 CGAP Kld11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23569	37170	1.64	2.4E+00	BE326702.1	EST_HUMAN	h63306.x1 NC1 CGAP Kld11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DEINITRIFICATION REGULATORY PROTEIN N1RQ
11335	24398	38047	1.36	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosomal DNA, region 76 degrees: gbpPFD operon end downstream
11640	24720	38413	2.44	2.4E+00	AF168652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApoSC) gene, ApoSC-c allele, complete cds
1282	14438	27507	8.88	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5967	10143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7612	20882	34168	2.76	2.3E+00	6078564	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7771	26221		2.37	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7838	21008	34518	1.28	2.3E+00	X60265.1	NT	M. mizsei drakJ and drakJ genes homologues coding for DnaK and DnaJ
8310	22388	36938	0.62	2.3E+00	6836317	NT	Polydorus ornithinilis mitochondrion, complete genome
8371	22446	36008	1.66	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
11041	24120	37768	2.72	2.3E+00	Q07078	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	2.3E+00	BF541887.1	EST_HUMAN	6020689121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
12075	25056	38764	2.14	2.3E+00	BF541887.1	EST_HUMAN	6020689121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
12445	25315	32091	7.41	2.3E+00	BE865237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
4126	17280	30276	1.06	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4432	17572	30554	4.12	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18858	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5458	18858	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5976	19160	32478	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-008 CT0254 Homo sapiens cDNA
5976	19160	32479	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-008 CT0254 Homo sapiens cDNA
6187	19363	32711	9.30	2.2E+00	BE290383.1	EST_HUMAN	600943-40111 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2869777 3'
6484	19651	33013	2.87	2.2E+00	Q00635	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN ML-2
6730	19893	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	19524		3.4	2.2E+00	AA594574.1	EST_HUMAN	N65802.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	z19704.1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	2d05g10.l1 Soares_tclat_N621F8_9w Homo sapiens cDNA clone IMAGE:786534 5'
7866	20820	34427	0.86	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8294	21376	34896	0.65	2.2E+00	BE301590.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2933207 3' similar to gb.D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
8294	21376	34897	0.65	2.2E+00	BE301590.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2933207 3' similar to gb.D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
9542	22807		12.40	2.2E+00	BE741678.1	EST_HUMAN	601504733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9768	28860		2.12	2.2E+00	Q04708	SWISSPROT	TRANSPONSON TY1 PROTEIN A
10269	23294	36860	1.12	2.2E+00	A1290373.1	EST_HUMAN	q166803.x1 Soares_placenta_21w6weeks_21w6HP606W Homo sapiens cDNA clone IMAGE:1803965 3' similar to gb.Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10269	23294	36861	1.12	2.2E+00	A1290373.1	EST_HUMAN	q166803.x1 Soares_placenta_21w6weeks_21w6HP606W Homo sapiens cDNA clone IMAGE:1803965 3' similar to gb.Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36841	3.04	2.2E+00	BF246782.1	EST_HUMAN	601555591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10673	23707	37315	2.8	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein RGR74 homolog mRNA, complete cds
11726	23912	37536	3.3	2.2E+00	P07911	SWISSPROT	URONOMULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THIP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	18016	28795	13.2	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449368.1	EST_HUMAN	U1H-B19-ek-9-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6260	19434		0.97	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20280	33688	3.51	2.1E+00	O70169	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dyx19c1, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20066	33468	5.88	2.1E+00	N28575.1	EST_HUMAN	W08a10.31 Soares melanocyte ZNF118 Homo sapiens cDNA clone IMAGE:270616 3' similar to gb:U55064
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM200671 5'
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dcdcl (DOKDEL) mRNA, complete cds
1366	14520	27585	1.37	2.0E+00	AF204627.1	NT	Homo sapiens p22Dcdcl (DOKDEL) mRNA, complete cds
1606	14750		3.09	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Nef-K+-ATPase beta 1 subunit mRNA, complete cds
2216	16360	28480	7.2	2.0E+00	Z76278.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	16360	28481	7.2	2.0E+00	Z76278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4216	17365	30363	1.71	2.0E+00	AW684498.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4216	17365	30354	1.71	2.0E+00	AW684498.1	EST_HUMAN	h113c05.31 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7722	20786		0.86	2.0E+00	P07586	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34815	4	2.0E+00	AB008678.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34816	4	2.0E+00	AB008678.1	NT	h113c05.31 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8214	21296	34817	4	2.0E+00	AB008678.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN G; MEMBRANE GLYCOPROTEINS E1 AND E2]
12815	26022	31670	6.76	2.0E+00	6834943	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32202	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32203	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6225	19400	32750	1.2	1.9E+00	BE969895.1	EST_HUMAN	HSPD22703 HMG Homo sapiens cDNA clone s4000117808
6702	19947		0.92	1.9E+00	AW845689.1	EST_HUMAN	Gallus gallus mitochondrion, complete genome
6888	20040		1.91	1.9E+00	Q89627	SWISSPROT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
8693	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
8863	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	601679636F1 NIH_MGC 78 Homo sapiens cDNA clone IMAGE:3946881 5'
8850	21638		3.32	1.9E+00	BF360208.1	EST_HUMAN	MFD-CT0063-071088-002-g02 CT0063 Homo sapiens cDNA
9096	22174		1.86	1.9E+00	O61781	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							CGM-MT0114-010600-323-h12 MT0114 Homo sapiens cDNA
							ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.9E+00	AA690125.1	EST_HUMAN	cd94404.s1 Stradiene lung (#637210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10760	23823	37447	0.67	1.9E+00	AF248280.1	NT	Homo sapiens g80-pro-pol precursor protein gene, partial cds
3162	16337	28346	1.69	1.9E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	28370	2.15	1.9E+00	U04355.1	NT	Synochococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	28371	2.15	1.9E+00	U04355.1	NT	Synochococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.9E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.9E+00	BF311989.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19682		1.28	1.9E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6879	20031	33441	1.15	1.9E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4198098 5'
7204	20069	33479	1.22	1.9E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.9E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,8-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE- (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.98	1.9E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8308	21390	34914	0.98	1.9E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9055	22134	36678	2.28	1.9E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.78	1.9E+00	R31042.1	EST_HUMAN	y172a08.l1 Scarsa placenta Nb2HP Homo sapiens cDNA clone IMAGE:136278 5'
9462	22518	36081	0.82	1.9E+00	AW880004.1	EST_HUMAN	QV6-QT0030-070300-149-a03 OT0030 Homo sapiens cDNA
9698	23034	36828	0.47	1.9E+00	P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36894	0.94	1.9E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10490	23525		4.71	1.9E+00	AF111849.1	NT	Homo sapiens PRO0630 mRNA, complete cds
10777	23810		0.75	1.9E+00	P44925	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	1.9E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12867	26444		6.01	1.9E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
13005	25887	31654	1.45	1.9E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1132	14297	27362	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUEROSE 6-FRUCTOSYL TRANSFERASE)
2345	15478	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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2445	15573	28702	1.49	1.7E+00	AI141067.1	EST_HUMAN	ox33705x1 Scarses_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4581	17718	30701	0.98	1.7E+00	Q80114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 8-FRUCTOSYL TRANSFERASE)
5730	18823	32216	1.73	1.7E+00	BE063548.1	EST_HUMAN	CN40-BT0282-171289-127 -05 BT0282 Homo sapiens cDNA
5730	18823	32217	1.73	1.7E+00	BE063548.1	EST_HUMAN	CN40-BT0282-171289-127 -05 BT0282 Homo sapiens cDNA
6141	19319	32661	3.02	1.7E+00	Q97T78	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6682	19940	33230	0.67	1.7E+00	P35916	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDP-C)]
7967	20448	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMID1 INTERGENIC REGION
7967	20448	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMID1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tcl1), mRNA
8252	21334	34852	0.61	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214069 5'
8739	21818	36382	0.76	1.7E+00	AF245613.1	NT	Hippoglossus hippoglossus Interferon inducible Mx protein (Mx) mRNA, complete cds
8828	21907	35519	1.63	1.7E+00	BF309000.1	EST_HUMAN	60189-4255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8901	21980	35519	0.68	1.7E+00	X68063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8901	21980	35520	0.68	1.7E+00	X68063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35833	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	23859	36981	2.44	1.7E+00	O60478	SWISSPROT	HOMEBOX PROTEIN DLX-3
9350	23859	36982	2.44	1.7E+00	O60478	SWISSPROT	HOMEBOX PROTEIN DLX-3
9806	22846		1	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10375	23410		0.54	1.7E+00	AW953981.1	EST_HUMAN	EST305751 IMAGE resequences, MAGC Homo sapiens cDNA
10857	23890	37609	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
10857	23890	37610	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
11898	24884	38582	1.67	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tap5091-cleaved sublibrary Homo sapiens cDNA not directional
12523	25356	32086	1.94	1.7E+00	AI678443.1	EST_HUMAN	tu22d07.x1 NCI_CGAP_Oes4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
2090	16230	28352	18.53	1.6E+00	AF198338.1	NT	MSR1 repetitive element
2101	16241	28362	4.14	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2107	16246	28367	1.26	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2357	16488		0.97	1.6E+00	X98373.1	NT	Mus musculus ST8GuaNacIII gene, exon 2
3026	16202	28225	1.22	1.6E+00	W59426.1	EST_HUMAN	Brn3ap gene encoding endo-polygalacturonase
							zid25f01.1 Scarses_fetal_NH1H10W Homo sapiens cDNA clone IMAGE:341688 5' similar to
							gb:D28805 N-ACETYL LAGTOSAMINE SYNTHASE (HUMAN);

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3857	17017		1.06	1.0E+00	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17204		6.05	1.0E+00	BF670077.1	EST_HUMAN	802188035T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310561 3'
4472	17012	30590	1.25	1.0E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17012	30591	1.25	1.0E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.0E+00	AF127897.1	NT	Salmonella typhimurium diffractin receptor (SBO27) gene, partial cds
5194	18316	31284	2.83	1.0E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5194	18316	31285	2.83	1.0E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5948	18134	32447	2.38	1.0E+00	LO4808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	18218	32540	0.78	1.0E+00	AF006681.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
6589	19759	33147	0.91	1.0E+00	BF380703.1	EST_HUMAN	IL2-UT0073-090900-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.0E+00	AW284881.1	EST_HUMAN	UHF-B12-alt-B-04-0-J1.s1 NCL CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33898	2.37	1.0E+00	BE697987.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8219	21301		1.3	1.0E+00	Q46378	SWISSPROT	VRULEXIN FACTOR MVN HOMOLOG
8574	21655	35196	3.3	1.0E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	36724	1.07	1.0E+00	11437222	NT	Homo sapiens hypothetical protein PRO0871 (PRO0871), mRNA
9101	22180	36725	1.07	1.0E+00	11437222	NT	Homo sapiens hypothetical protein PRO0871 (PRO0871), mRNA
9272	22348	36898	0.49	1.0E+00	BE388331.1	EST_HUMAN	801283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3005947 5'
9659	25957	34615	1.05	1.0E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9659	25957	34616	1.05	1.0E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9786	26326		0.7	1.0E+00	AF043403.1	NT	Thermotoga maritima ethanolic D-xylose-binding protein (xyf) gene, complete cds
9935	22974	36566	1.49	1.0E+00	T41280.1	EST_HUMAN	ph868_191TV Outward AU-paired hncDNA library Homo sapiens cDNA clone ph868_191TV
10388	23423	37029	1.09	1.0E+00	AW635844.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10388	23423	37030	1.09	1.0E+00	AW635844.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10552	23987	37195	0.52	1.0E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37726	1.77	1.0E+00	P64817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11082	18218	32540	4.8	1.0E+00	AF005631.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
12006	24691	38695	3.68	1.0E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	28275	2.95	1.0E+00	U63449.1	NT	Rattus norvegicus Jun dimerization protein 2 (jdp-2) mRNA, complete cds
241	13463	28492	2.44	1.0E+00	AED02201.2	NT	Chlamydomonas reinhardtii AF389, section 32 of 94 of the complete genome
636	13821		1.81	1.0E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2481	15608	28732	1.66	1.0E+00	AJ1131402.1	NT	Potato Virus A RNA complete genome, isolate U
2584	16709	28828	2.02	1.0E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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3208	16608	28732	1.75	1.5E+00	AJ131402.1	NT	Prdoto virus A RNA complete genome, isolate U
3482	16820	20840	0.77	1.5E+00	AE001946.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5846	18036	32942	0.71	1.5E+00	AI658301.1	EST_HUMAN	U12F10.X1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
5946	19036	32943	0.71	1.5E+00	AI658301.1	EST_HUMAN	U12F10.X1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
6536	19889	33072	2.43	1.5E+00	R17879.1	EST_HUMAN	Y010e02.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 5'
7278	20361		1.68	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33853	18.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA888259.1	EST_HUMAN	ak20710.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	ar07b11.s1 Strategene echino brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gds:595936 SEROTRANSFERRIN PRECURSOR (HUMAN)
8313	21395	34820	0.9	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8397	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21825	35463	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8218	22286		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35863	0.51	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096135 5'
9884	22733	36303	0.85	1.5E+00	R81828.1	EST_HUMAN	Y03101.1 Scores placenta NK2HP Homo sapiens cDNA clone IMAGE:147687 5'
9835	22876	36458	1.5	1.5E+00	AW375687.1	EST_HUMAN	QV3-CT0162-281089-008-009 CT0162 Homo sapiens cDNA
10064	23102	36705	8.49	1.5E+00	BF378754.1	EST_HUMAN	RC0-TN0078-150800-034-g05 TN0078 Homo sapiens cDNA
10258	23283		1.86	1.5E+00	BF337944.1	EST_HUMAN	602035577F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183865 5'
10369	23434	37040	2.28	1.5E+00	AA017689.1	EST_HUMAN	zs89g06.1 Scores retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
10369	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	zs89g06.1 Scores retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
11684	24683	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hbf1) Homo sapiens cDNA clone DKFZp547P243 3'
11894	24823		7.68	1.5E+00	X07380.1	NT	Maize mitochondrial RNA-Ser gene and tRNA-Phe pseudogene
11829	24915	38817	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94d08.x1 NCL_CGAP_G11.1 Homo sapiens cDNA clone IMAGE:2116433 3'
11829	24916	38818	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94d08.x1 NCL_CGAP_G11.1 Homo sapiens cDNA clone IMAGE:2116433 3'
12515	26066	31682	1.81	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12705	25508		3.82	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genomes segment 3/6
12888	25589		2.17	1.5E+00	6878482	NT	Rattus norvegicus 5'-Lipoxygenase (Alox5), mRNA
13220	25704	31888	1.31	1.5E+00	BF223035.1	EST_HUMAN	7q82d08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13288	26271	2.27	1.4E+00	7681685	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
30	13288	26272	2.27	1.4E+00	7681685	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glmA) gene, complete cds
2411	15541		9.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15551	28954	1.7	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	28055	3.22	1.4E+00	AF064594.2	NT	Fugu rubripes neurofibromatosis type 1 (NF-1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064594.2	NT	Fugu rubripes neurofibromatosis type 1 (NF-1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16553		0.79	1.4E+00	6483733	NT	Homo sapiens Mac4 homolog (MAD4) mRNA
4370	17513	30483	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMD-NN1005-140300-286-108 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMD-NN1005-140300-286-108 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297566 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18687	31705	1.73	1.4E+00	AW064978.1	EST_HUMAN	wk45g07.x1 NCL_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2510480 3'
5945	18839		6.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1167 protein, partial cds
6408	19578	32839	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	26214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II
6861	20189	33614	0.8	1.4E+00	AW893057.1	EST_HUMAN	CMS-NN0008-300300-132-bt12 NN0008 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133268.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7454	20631	34005	1.14	1.4E+00	AW467780.1	EST_HUMAN	ha23105.X1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element
7514	20588	34062	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7514	20588	34063	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8530	21611		0.72	1.4E+00	P07693	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8894	22073		6.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudosubterminal region; segment 1/2
9295	22371	35020	1.65	1.4E+00	R20459.1	EST_HUMAN	yg33112.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9398	22472	36038	3.83	1.4E+00	BE084887.1	EST_HUMAN	RC1-BT0313-301299-012-105 BT0313 Homo sapiens cDNA
9432	22506	36072	0.65	1.4E+00	AF194844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.86	1.4E+00	BF075545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288197 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL6-HT0188-291089-008 C04 HT0188 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL6-HT0188-291089-008 C04 HT0188 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D03441.1	NT	Pandorina cokerianae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D03441.1	NT	Pandorina cokerianae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23885	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11489	24507	38232	4.52	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11681	24689	38379	3.46	1.4E+00	BE962107.2	EST_HUMAN	801055184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3945905 3'
11681	24689	38380	3.46	1.4E+00	BE962107.2	EST_HUMAN	801655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3945905 3'
11711	24751	38444	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.99	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen ss70-2 (SE70-2), mRNA
594	13776		1.98	1.3E+00	Z73840.1	NT	M. musculus gene encoding 4-Dihydroxyethyl-bisphosphate dehydrogenase
825	14100	27164	2.79	1.3E+00	AJ271182.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative psfH-HbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27649	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27650	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 167 (HZF22) (ZNF167) mRNA
1387	14642		0.98	1.3E+00	U61730.2	NT	Cdx lacryme-jabi dihydrodipicolinate synthase (dsapA) gene, complete cds
1641	14783		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2815	15739		1.81	1.3E+00	BE960735.2	EST_HUMAN	801061233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915845 3'
3005	16180	28201	0.96	1.3E+00	6756921	NT	Mus musculus alpha-spectrin 1, erythroid (Spnat1), mRNA
3886	16849	28857	1.14	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5631	18825	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5927	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32682	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMD-CT0289-261198-004-008 CT0289 Homo sapiens cDNA
6142	19320	32683	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMD-CT0289-261198-004-008 CT0289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M59498.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6880	20042		0.71	1.3E+00	Q00166	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P46940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7092	20186	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447885 5'
7249	20332	33779	0.98	1.3E+00	BE243671.1	EST_HUMAN	TCBAP1D0659 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP Homo sapiens cDNA clone TCBAP0659
7616	20686	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21575	35112	1.78	1.3E+00	AJ003912.1	NT	Sus scrofa pig gene
8642	21722	36269	2.28	1.3E+00	BE989379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866185 3'
8758	21837	36376	1.05	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3960832 3'
8807	21888		1.87	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8890	22069	35609	0.88	1.3E+00	A827629.1	EST_HUMAN	wc85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
8947	22423	36976	0.61	1.3E+00	H42881.1	EST_HUMAN	y068c03.s1 Soares breast 3NH-Bist Homo sapiens cDNA clone IMAGE:183078 3'
8947	22423	36977	0.61	1.3E+00	H42881.1	EST_HUMAN	y068c03.s1 Soares breast 3NH-Bist Homo sapiens cDNA clone IMAGE:183078 3'
9715	22760		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylaseN-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S. alba pfr-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S. alba pfr-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF059250.1	NT	Homo sapiens lipovigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	w03103.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2528477 3' similar to gb.M31522
9871	22911	36496	1.65	1.3E+00	O00764	SWISSPROT	TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9952	22991	36584	1.21	1.3E+00	A827628.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMMAN)
10031	23059	36668	0.88	1.3E+00	AJ223082.1	NT	w085a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482100 3'
10031	23059	36669	0.88	1.3E+00	AJ223082.1	NT	Lactobacillus lactis cremoris NCDO-1191 chromosomal inversion junction DNA
10070	23108	36711	3.93	1.3E+00	BE963378.2	EST_HUMAN	Lactobacillus lactis cremoris NCDO-1191 chromosomal inversion junction DNA
10130	23168		0.57	1.3E+00	AJ555944.1	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866185 3'
10353	23388	36906	0.5	1.3E+00	AF061251.1	NT	1q7/r12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb.X14723
10353	23388	36907	0.5	1.3E+00	AF061251.1	NT	GLJLISTERIN PRECURSOR (HUMAN);
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10435	23470	37076	1.59	1.3E+00	M228853.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10811	23844		0.99	1.3E+00	AL163302.2	NT	Vibrio cholerae chromosome II, section 49 of 53 of the complete chromosome
10838	23871	37463	0.47	1.3E+00	A890848.1	EST_HUMAN	Campylobacter jejuni kenamorph phosphotransferase (aphA-7) gene, complete cds
10851	23884		0.53	1.3E+00	8923637	NT	Homo sapiens chromosome 21 segment H821C102
							w032a10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498822 3' similar to SW:TR08_HUMAN
							Q16881 THIOREDOXIN REDUCTASE;
							Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

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Probe SEQ ID NO.:	Exon SEQ ID NO.:	ORF SEQ ID NO.:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7849159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7849159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3Nb1-Bst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3Nb1-Bst Homo sapiens cDNA clone IMAGE:183076 3'
10832	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25239	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z16832.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	xp08ac03.x1 NCI_CGAP_HiHo Homo sapiens cDNA clone IMAGE:2739888 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11823	24809	38610	2.28	1.3E+00	Z68882.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
11994	24979		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketoadyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12604	26347		3.81	1.3E+00	AF187873.1	NT	Caenia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	26485	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	80223185F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	26589		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRUX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	26549		1.53	1.3E+00	AF187035.1	NT	Sturmia illium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	26783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium Bn6 2,3-dihydroxyphenyl dioxygenase (hprCII) gene, complete cds
13231	26981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
687	13853	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	z22408.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431635 3'
846	14024	27082	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
846	14024	27083	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
846	14024	27084	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
901	14078		1.21	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AL262242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AL262242.1	NT	pea seed-borne mosaic virus complete genome
2066	16207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	28359	1.08	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	28421	7.01	1.2E+00	AL161683.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	28422	7.01	1.2E+00	AL161683.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16630		3.57	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TREB PRECURSOR
3437	16805	28625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16864	28687	9.16	1.2E+00	U75802.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FTD175-050800-203-g08_1_F10175 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16005	28625	1.06	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4504	17731		1.91	1.2E+00	AB07060.1	NT	Rattus rattus cardiac A23 gene, exons 1-23
4645	17781	30763	0.94	1.2E+00	AL161609.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30805	2.03	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T. plinatum chloroplast 16S gene, partial
5554	18761	31798	1.13	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18868	32162	2.34	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c06 ST0191 Homo sapiens cDNA
5917	19105		0.65	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
6096	19180	32602	0.77	1.2E+00	AF016032.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6260	19454	32802	2.45	1.2E+00	X74885.1	NT	D. hydei ay1 repeat cluster DNA, fragment D
6342	19512	32859	3.61	1.2E+00	BE003113.1	EST_HUMAN	QY4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19689	32953	1.28	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
6420	19588	32954	1.28	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
6463	19630	32991	36.06	1.2E+00	AA789254.1	EST_HUMAN	afB4g12.a1 Scores_testis_NIT Homo sapiens cDNA clone 1322374 3'
							y689b12.s1 Scores melanocyte ZNF191 Homo sapiens cDNA clone IMAGE:273598 3' similar to gbM87635j1-HUMAAU472 Human carcinoma cell-derived Alu RNA transcript, (fRNA); gbJ04970
6598	19728	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6630	19780	33178	0.62	1.2E+00	P17671	SWISSPROT	ECDOSE-INDUCIBLE PROTEIN E75-A
6634	19783	33182	1.94	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7055	20108	33624	1.72	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7067	20120	33634	2.61	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	zq38105.l1 Stratagene hNT neuron (8837253) Homo sapiens cDNA clone IMAGE:632001 5' similar to gbD10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7403	20481		0.71	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7542	20847	34092	1.85	1.2E+00	AV734595.1	EST_HUMAN	AV734595 cDNA Homo sapiens cDNA clone cdAAFH03 5'
7828	20863	34386	2.91	1.2E+00	X74207.1	NT	L. lactis pyd and pyrf genes
7897	21047	34560	0.6	1.2E+00	BE787848.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8767	21846	35367	3.19	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8863	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	Homo sapiens CGH-30 protein (LOC51011), mRNA
9077	22156		0.7	1.2E+00	7706271	NT	MR2-CT0222-201068-001-e07 CT0222 Homo sapiens cDNA
9228	22304	35847	1.81	1.2E+00	AW377210.1	EST_HUMAN	y689a08.l1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'
9440	22514	36078	0.61	1.2E+00	H48596.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID N :	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9598	22853	38224	3.78	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845	38423	2.13	1.2E+00	D11745.1	EST_HUMAN	HJMH101A01 Liver HepG2 cell line. Homo sapiens cDNA clone hnt01a01
10135	23173	38771	3.6	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10532	23307		0.82	1.2E+00	AB000866.1	NT	Homo sapiens Notho gene, exon 1
11432	24483	38158	1.69	1.2E+00	M38688.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0284-161188-001-c01 ST0284 Homo sapiens cDNA
11688	24743		7.69	1.2E+00	BE160781.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23630	37556	3.13	1.2E+00	U50147.1	NT	Radix norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Metazoa mitochondrial F-O-A-TPase proteolipid (subunit 8) gene
12471	25384	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 8/14
13218	25703		2.68	1.2E+00	AA077803.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
478	13671	28703	1.11	1.1E+00	D88980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14851	28045	1.23	1.1E+00	AW895888.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575889.1	EST_HUMAN	UJHF-BR0p-alk-F02-0-UJ.s1 NIH_MGC 52 Homo sapiens cDNA clone IMAGE:3074834.3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Galus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	28584	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	28596	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	16740	29757	1.02	1.1E+00	8822841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
							wf6-4h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2859461.3' similar to
3670	16833	28844	0.88	1.1E+00	AI808360.1	EST_HUMAN	SW_F531_HUMAN_Q12868_P53-BINDING PROTEIN 53BP1 ;
3812	16972	28974	1.16	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3812	16972	28975	1.16	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3820	17078		0.92	1.1E+00	X86374.1	NT	H-parasaccharomyces hphim(A), hphim(C), hphIR and menB genes
4054	17210	30220	1.03	1.1E+00	8822841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4130	17283	30278	0.72	1.1E+00	6765206	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4331	17474		6.82	1.1E+00	5835331	NT	R. uniconis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
5180	18302	31266	2.08	1.1E+00	X78425.1	NT	E. faecalis pfp5 gene
5422	18323	31588	1.49	1.1E+00	6978530	NT	Radix norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18324	32218	14.33	1.1E+00	BE980184.1	EST_HUMAN	601652778R1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3825835.3'
5750	18342	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738280.3'
6217	19382	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter), member 14 (SLC8A14), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6404	19578	32835	0.69	1.1E+00	AF167861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	1.1E+00	R06037.1	EST_HUMAN	y88a03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124924 5'
6856	20008	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7447	20524	33997	0.58	1.1E+00	X55981.1	NT	Malva mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.67	1.1E+00	BF683714.1	EST_HUMAN	602136978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20728	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20728	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.36	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25553	34305	1.04	1.1E+00	11987880	NT	Mus musculus silent mating type information regulation 2, (S.oarevles), homolog, like (Sir2), mRNA
8325	21407	34094	3.2	1.1E+00	BF693936.1	EST_HUMAN	602082592F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8416	21497	35029	0.91	1.1E+00	AJ478339.1	EST_HUMAN	hm39h11.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8835	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
9015	22084	35834	0.87	1.1E+00	S80750.1	NT	VI-Har18-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region (human, mRNA Partial, 376 nt)
9126	22205	35748	0.53	1.1E+00	A079946.1	EST_HUMAN	cc34f05.x1 Soares_NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080	36450	0.75	1.1E+00	BE384878.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3817418 5'
9828	22868	36450	0.61	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9883	22923		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9874	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10038	23078	36676	1.86	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
10141	23179	36777	4.08	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Grg3), mRNA
10719	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23854	37488	0.56	1.1E+00	AB178821.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10822
10886	23970	37600	1.97	1.1E+00	11087964	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN); Homo sapiens KIAA0826 gene product (KIAA0826), mRNA
10947	24029		3.14	1.1E+00	AF068942.1	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11343	24408	38055	3.72	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P450C8 (CYP2C8) gene, 5' flank and exon 1
11361	18489		2.74	1.1E+00	8822873	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ D NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11368	24427	38083	2.83	1.1E+00	AF012802.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11369	24427	38084	2.03	1.1E+00	AF012802.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38408	3.88	1.1E+00	AB009689.1	EST_HUMAN	w766r1.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	24858	38502	1.38	1.1E+00	D88501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D88501.1	NT	Human PBI gene, complete cds
12441	25312		1.82	1.1E+00	P07686	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	25371	32070	3.56	1.1E+00	AF210698.1	NT	Taenia solium immunogenic protein Ts78 mRNA, partial cds
12680	25980		1.86	1.1E+00	AF234189.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	13347	26374	2.1	1.0E+00	D88425.1	NT	Canis cubana mRNA for sarcolemmal kinase, complete cds
431	13628		-2.78	1.0E+00	AB021094.1	NT	Mercurialis polymorpha gene for 28S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
690	13781	26800	1.44	1.0E+00	AJ251690.1	NT	Stardlia ligula mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13879		2.29	1.0E+00	AF125894.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1785	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15578	28903	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	15578	28904	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA028453.1	EST_HUMAN	af28908.e1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204 ; contains element MER22 MER22 MER22 repetitive element ;
2840	16117	28129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2840	16117	28130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.95	1.0E+00	O14228	SWISSPROT	HYPOPHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3289	16443	29463	1.16	1.0E+00	AA028453.1	EST_HUMAN	af28908.e1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204 ; contains element MER22 MER22 MER22 repetitive element ;
3459	16828		0.73	1.0E+00	AF222781.1	NT	Rattus norvegicus neurokinin U precursor (NmU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	28939	1.61	1.0E+00	AJ223816.1	NT	Agerium bisporus mRNA for tyrosinase

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4180	17330	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4380	17633		0.72	1.0E+00	8222245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31598	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine protease
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus intramolecular calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus intramolecular calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	18259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
8248	19422	32768	1.87	1.0E+00	AW452782.1	EST_HUMAN	UH-H-B13-ab-d-09-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068886 3'
8818	19778	33187	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
8871	19830	33219	0.83	1.0E+00	AF104680.1	NT	Homo sapiens cell cycle protein (PA204) gene, exons 2 through 5
8767	19828		1.07	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6795	19950	33349	0.82	1.0E+00	BE797710.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6795	19950	33350	0.82	1.0E+00	BE797710.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6916	20231	33684	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxaprin
7288	20371	33820	1.15	1.0E+00	S62770.1	NT	Insulin-like growth factor-binding protein 4 [catilla, pulmonary artery endothelial cells, mRNA, 2028 nt]
7847	20716		9.08	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34462	8.02	1.0E+00	AA776191.1	EST_HUMAN	ac70b08.s1 Strabegene lung (8337210) Homo sapiens cDNA clone IMAGE:868781 3'
8019	21070		0.72	1.0E+00	BF79213.1	EST_HUMAN	602163782F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284727 5'
8148	21230	34749	1.85	1.0E+00	BE888267.1	EST_HUMAN	601443850F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8148	21230	34760	1.86	1.0E+00	BE888267.1	EST_HUMAN	601443850F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8335	18408		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21828	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21828	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8672	21762		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.54	1.0E+00	Q876T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21788	35322	0.54	1.0E+00	Q876T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	25858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-H10228-181089-011-e06 H10228 Homo sapiens cDNA
8778	21855	35307	1.15	1.0E+00	U42720.2	NT	Sin18 Immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes. >
8822	22001	35540	1.8	1.0E+00	M39427.1	NT	Human immunodeficiency virus type 1 (HIV-1). Isolate SF33.
8471	22528	35081	1.95	1.0E+00	BE807592.1	EST_HUMAN	601497581F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3890421 5'
9682	22731	36301	1.82	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9682	22731	36302	1.82	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9810	22850	36429	1.81	1.0E+00	AV688554.1	EST_HUMAN	AV688554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44962.1	NT	Xenopus laevis zona pellucida G glycoprotein precursor (XZPG) mRNA, complete cds
9815	22855	36435	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida G glycoprotein precursor (XZPG) mRNA, complete cds
10318	23353	36961	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10318	23353	36962	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10408	23443	37060	0.69	1.0E+00	A077620.1	EST_HUMAN	OY15007.s1 Soares_senescent_fibroblasts_NHFSF Homo sapiens cDNA clone IMAGE:1065901 3'
10633	23668	37176	3.69	1.0E+00	AV768825.1	EST_HUMAN	AV768825 BM Homo sapiens cDNA clone BMFAW04 5'
10694	23727	37333	19.71	1.0E+00	AA004882.1	EST_HUMAN	Zf94a02.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10694	23727	37334	19.71	1.0E+00	AA004882.1	EST_HUMAN	Zf94a02.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10728	23761	37368	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exon 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	S80825.1	NT	PBR1=proline-rich protein [intron 3] [human, Genomic, 898 nt]
11342	24405	38054	1.48	1.0E+00	AA701404.1	EST_HUMAN	Zf63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436463 3' similar to contains AU repetitive element; contains element MEF38 repetitive element;
11825	24814		1.82	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
12328	25238		5.49	1.0E+00	P19309	SWISSPROT	THROMBOMODULIN PRECURSOR (PETOMODULIN) (TM)
12878	25451		2.67	1.0E+00	AW976184.1	EST_HUMAN	EST388283 IMAGE rescues, MAGN Homo sapiens cDNA
3693	18855		1.04	9.9E-01	AF174595.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5752	18944	32246	8.8	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6990	19176	32498	0.83	9.9E-01	Q09032	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.9E-01	U86687.1	NT	Lycopodium obscurum putative MIT copy 1 nematode-resistance gene
9765	22693		2.14	9.9E-01	Q28942	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26753	1.17	9.8E-01	P22967	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	16976		1.29	9.8E-01	AF174844.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3803	17062	30061	0.67	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839461 3'
3903	17062	30062	0.67	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839461 3'
7349	20429	33960	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JN883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JN883
7349	20429	33961	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JN883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JN883
7823	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7823	20878	34379	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21985	35534	0.94	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23687		1.02	9.8E-01	AA825595.1	EST_HUMAN	cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE268705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE268705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CTR1), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33951	2.73	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.9	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.7E-01	M00544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35691	0.73	9.7E-01	BE799822.1	EST_HUMAN	601932165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	BF511208.1	EST_HUMAN	UH-B14-act-9-07-UJ1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25780		3.17	9.7E-01	AL114281.1	NT	Bovitis chitrea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696	30676	0.74	9.6E-01	AF197825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17696	30676	0.74	9.6E-01	AF197825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4590	17717	30700	1.28	9.6E-01	AW789874.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5872	19062	32369	3.51	9.6E-01	Z70568.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2884
5872	19062	32370	3.51	9.6E-01	Z70568.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2884
6886	20038	33447	0.6	9.6E-01	Z97941.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7612	20586	34059	0.63	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (P8) mRNA, complete cds
8588	21867		1.62	9.6E-01	X85276.1	NT	P. falciparum complete gene map of plasmid-like DNA (IR-A)
9052	22191	35675	0.92	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
11346	24408	38090	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11808	24798	38406	3.91	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NP0 Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	38497	3.91	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NP0 Homo sapiens cDNA clone NPDBAG06 5'
12225	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centromeres protein 2 (CEP2), mRNA
12916	26061	31686	1.68	9.6E-01	U91423.1	NT	Sphynx tibu NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15970	28794	1.61	9.5E-01	7705581	NT	Homo sapiens C3H-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.6E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
3882	17041	30039	2.1	9.6E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
9202	22280	35819	0.71	9.5E-01	A1190162.1	EST_HUMAN	q657d07.x1 Score testis NIH Homo sapiens cDNA clone IMAGE:1733581 3'
9306	22382	35933	1.04	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0286-241199-011-502 CT0286 Homo sapiens cDNA
11520	24576	38254	1.56	9.5E-01	BF216771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	9.5E-01	AW233789.1	EST_HUMAN	UJH-B12-afp-f03-0-UJ.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16446		5.72	9.4E-01	AF165890.1	NT	Bartonella clamydiae RNA polymerase beta subunit (pob) gene, partial cds
3289	16463		2.17	9.4E-01	AF080656.1	NT	Pimpriella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8008	22145	35682	0.79	9.4E-01	M80724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
12498	25343		1.86	9.4E-01	BE781281.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868828 5'
12614	25975		1.4	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phytoey-CoA hydrolase (PHYH) gene, exon 5
2689	15818	28834	3.62	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4146	17288	30289	0.86	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
4146	17288	30290	0.86	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
6709	18302	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6786	18368	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7486	20361		1.08	9.3E-01	AF270648.1	NT	Plasmodium falciparum murene parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	9.3E-01	AA847040.1	EST_HUMAN	cc091603.s1 NCI CGAP_O2 Homo sapiens cDNA clone IMAGE:1385357
8013	22092		1.1	9.3E-01	AF081981.1	NT	Xenopus laevis CCH1 zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8137	22216	35780	0.89	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	25883	31881	2.09	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (IPPR2), mRNA
13049	25888		1.22	9.3E-01	AF271207.1	NT	Acades trisartus putative large subunit ribosomal protein rpl.34 mRNA, complete cds
3311	18484	28605	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4899	18128		0.81	9.2E-01	BF128873.1	EST_HUMAN	601817814F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	18025		1.58	9.2E-01	7106410	NT	Mus musculus scute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	18289	32824	4.97	9.2E-01	BF037588.1	EST_HUMAN	601401153F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3684081 5'
6770	18925	33320	0.85	9.2E-01	M84703.1	NT	N. crassa vsh1-RNA synthetase (cyl-20/un-3) gene
9860	22800	38484	0.88	9.2E-01	AL161688.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9849	22888	38582	1.31	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430983	NT	Homo sapiens lysosomal enzyme-like protein 1 (LALP1), mRNA
10827	23881	37289	1.64	9.2E-01	BF583251.1	EST_HUMAN	7058403.x1 NCI CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW_AU56M_TRYBB
10883	23967	37698	1.78	9.2E-01	BE583811.1	EST_HUMAN	P04840 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
							601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1654	14807	27892	1.82	9.1E-01	T98875.1	EST_HUMAN	ye52f01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121389 3' similar to contains
2183	15328		1.49	9.1E-01	8823058	NT	Alu repetitive element
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	16449	28488	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200389 Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB20038 5'
3275	16449	28489	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200389 Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB20038 5'
8286	18489	32824	1.84	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8635	18794	33183	3.25	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7750	20810	34300	17.48	9.1E-01	AA806823.1	EST_HUMAN	cd71g08.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336882 3'
7916	20567	34473	2.81	9.1E-01	U72885.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10378	23414	37028	0.6	9.1E-01	P38432	SWISSPROT	P80-COILIN
12565	26064		19.87	9.1E-01	AF060113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	16451	29472	0.8	9.0E-01	7881023	NT	Homo sapiens DKFZP684M2423 protein (DKFZP684M2423), mRNA
3439	16807		0.73	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17888	30857	0.88	9.0E-01	8022310	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4498	17838	30820	1.43	9.0E-01	AF098810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
5127	18252	31218	13.05	9.0E-01	AF017729.1	NT	Oryzobagus cuticulus Rad51 (RAD51) mRNA, complete cds
7551	20823	34100	0.82	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7579	20651		1.42	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID N :	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9549	22614	36163	0.68	9.0E-01	AF086791.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
10035	23073	36873	0.48	9.0E-01	U89702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146733.2	NT	Mus musculus neurexin U precursor (Nrxu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PF-T27 (PF-T27) gene, complete cds; and H1AR (H1ar) gene, complete cds
5814	19004	32309	2.5	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6378	19647	32309	1.28	8.9E-01	X60988.1	NT	Rabbit MHC fragment RLAD-F DNA
6590	25627	33134	0.82	8.9E-01	BF217838.1	EST_HUMAN	601882708F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	25627	33135	0.82	8.9E-01	BF217838.1	EST_HUMAN	601882708F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.82	8.9E-01	AF259887.1	NT	Citrona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12423	25300	30786	4.02	8.9E-01	AE002188.2	NT	Chlamydia pneumoniae AF39, section 21 of 84 of the complete genome
4584	17769	30786	2.11	8.8E-01	O268360	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18938	31706	0.68	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7701	20768	34250	0.59	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10438	23471	37077	1.07	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11337	24400	38048	2.23	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	25072	38779	7.56	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to centaine Alu repetitive element/contains element MER22 repetitive element;
12240	29158	38779	2.13	8.8E-01	D60911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576583-1718643
477	19372	28704	2	8.7E-01	AF108833.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2475	19502	28727	0.98	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2838	16115	28127	5.32	8.7E-01	AA596863.1	EST_HUMAN	nm05f11.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18246		4.12	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa lipotease (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-hatbenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-hatbenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
8229	21311	34831	0.66	8.7E-01	AW697335.1	EST_HUMAN	RCA-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9130	22209	35752	0.66	8.7E-01	AL239456.1	EST_HUMAN	gh36e03.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9130	22209	35753	0.66	8.7E-01	AL239456.1	EST_HUMAN	gh36e03.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9339	22378	38568	2.07	8.7E-01	AE004063.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10511	23546	37159	1.08	8.7E-01	BF670183.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309808 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10611	23648	37167	1.08	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QV0-NIN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107694.1	EST_HUMAN	6018223884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12034	25017	38721	3.32	8.7E-01	BF107694.1	EST_HUMAN	6018223884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12852	25940		2.8	8.7E-01	AV681898.1	EST_HUMAN	AY661898 GLC Homo sapiens cDNA clone GLCGY307 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGFBP gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W68088.1	EST_HUMAN	z444603.1 Scoville_fetal heart NBH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01		NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16874	28873	0.85	8.6E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster marlin (Orserlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60647.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S78772.1	NT	polyprotein [Cassacke B4 virus GB4, host-mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33408	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
7898	20761		0.64	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AF001518.1	NT	Bacillus halodurans genome DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collagen response mediator protein (CRMP) mRNA, complete cds
9887	22027		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12856	25883		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.49	8.5E-01	AL011824.1	NT	Arabidopsis thaliana (ecotype Columbia) sp2 gene, exons 1-6
6866	20018	33427	1.1	8.5E-01	AF185214.1	NT	Bacteriophage D3, complete genome
7894	20759	34243	2.38	8.5E-01	BE642612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3435505 5'
8180	21282	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8813	21693	35230	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
6702	21782	36315	0.68	8.5E-01	AL243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
10558	23593	37198	1.49	8.5E-01	AB006798.1	NT	Gynerium caldarium gene for SlgC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006798.1	NT	Gynerium caldarium gene for SlgC, complete cds
12577	25056		5.29	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9607008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30898	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7881	21041	34553	0.67	8.4E-01	AF061142.1	NT	Manesha brassicae phenolase binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
760	13941	26388	2.17	8.3E-01	M63437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.46	8.3E-01	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010878.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
6383	16886	31484	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AJ791952.1	EST_HUMAN	nm011212.y6 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.H1 THR repetitive element:
10318	23351	36958	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23984	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 149) of the complete genome
10930	24012		1.65	8.3E-01	Z712472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	9.85	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	16249	28368	2.72	8.2E-01	AB000493.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2158	15282		1.32	8.2E-01	AF145598.1	NT	Mus musculus trophinin (Tm) gene, complete cds
2744	15861		0.95	8.2E-01	AW376590.1	EST_HUMAN	IL3-CT0219-161198-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4247	17368	30381	0.7	8.2E-01	Z72884.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062W
4247	17368	30382	0.7	8.2E-01	Z72884.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062W
5217	18338	31311	1.19	8.2E-01	AB000488.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	19338	33332	0.69	8.2E-01	X96283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6781	19338	33333	0.69	8.2E-01	X96283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6813	20228	33661	0.76	8.2E-01	AJ010142.1	NT	Arenaria muscaria mRNA for SCIL25 protein
7037	20173	33696	3.19	8.2E-01	AW378433.1	EST_HUMAN	CH4-HT0243-081188-037-e01 HT0243 Homo sapiens cDNA
7419	25944	33980	4.48	8.2E-01	Z12128.1	NT	S. cerevisiae MET1, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8039	21719	35256	0.55	8.2E-01	BE283145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23268	36856	0.81	8.2E-01	AB014630.1	NT	Homo sapiens mRNA for KIAA0690 protein, partial cds
10264	23269	36897	1.51	8.2E-01	AF052858.1	NT	Homo sapiens thiorodan-related protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38459	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
11772	24764	38460	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
12803	26221	32102	2.22	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
181	13404		2.02	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
289	13516	28649	10.2	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
2003	16233		1.95	8.0E-01	BE530982.1	EST_HUMAN	602072473F1 NCI CGAP_Bim7 Homo sapiens cDNA clone IMAGE:4215091 5'
3146	16322	28334	1.32	8.0E-01	AF127897.1	NT	Scimitril batifensis olfactory receptor (SBO27) gene, partial cds
3387	16557	28572	1.29	8.0E-01	AB006183.1	NT	Mus musculus gene for octadecyl glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	X83738.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5086	18224	31196	1	8.0E-01	7657362	NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21261		2.68	8.0E-01	AW601489.1	EST_HUMAN	RCO-NN1012-270300-021-108 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11035.1	NT	Rice stripe virus RNA 3'
10836	23669		0.48	8.0E-01	BE833328.1	EST_HUMAN	QV3-OT0085-280800-250-c08 OT0085 Homo sapiens cDNA
10827	23680	37483	0.48	8.0E-01	AB045587.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24287	37602	1.43	8.0E-01	Q62783	SWISSPROT	CREB-BINDING PROTEIN
468	13681	28697	0.75	7.9E-01	DT1476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
793	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1887	14839		1.08	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	15468	28603	9.03	7.9E-01	AB004816.1	NT	Cryptosporidium parvum section 54 of 163 of the complete genome
2338	15469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3805	16769	28784	3.57	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17557		0.87	7.9E-01	BE268612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635785 5'
4734	17869	30852	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4734	17869	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.68	7.9E-01	6753753	NT	Mus musculus embigin homolog (Drosophila) (Emh), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5235	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.68	7.9E-01	AF138718.1	NT	Chryseomys bezziana peritrophin-48 precursor, gene, complete cds
6475	18942	33003	0.68	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34603	2.66	7.9E-01	X80898.1	NT	P. sativum GR gene
9747	22811	36890	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10265	23290	36887	5.43	7.9E-01	IP19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10288	23331	36834	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GK Homo sapiens cDNA clone GKCDRE12 3'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, cTDP-4-hydro-L-rhamnose reductase, complete cds
10845	23878	37498	0.61	7.9E-01	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11259	24325		1.75	7.8E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.94	7.8E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
889	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC1K-H041 normalized infant brain cDNA Homo sapiens cDNA clone c-1k104
2349	15480	28612	6.99	7.8E-01	AW059567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17958	30942	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Ucd5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6194	18370	32721	2.28	7.8E-01	AF115858.1	NT	Sphenodon punctatus alpha endolase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6691	19761	33136	0.84	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8088	21768	35289	1.13	7.8E-01	BF106927.1	EST_HUMAN	715405x1 Soares NSF F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D.discoideum recGAP gene
9633	22688	36170	0.56	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAN) (NUP214), mRNA
10329	23364		1.28	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MOL-ALPHA1)
12571	28033		1.82	7.8E-01	L28280.1	NT	Arabidopsis thaliana 1-aminino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	28403	5.78	7.7E-01	AF184945.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	13925		1.72	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAsalpha) and major histocompatibility protein class II beta chain (IAbeta) genes, complete cds; butyrophilin-like (NCG), butyrophilin-lt>
2776	15892	28003	1.34	7.7E-01	O38916	SWISSPROT	CITRATE SYNTHASE
3438	16806		0.88	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-7) (GALNAC-T7), mRNA
3689	16851	28859	3.96	7.7E-01	AF118085.1	NT	Homo sapiens PRO1875 mRNA, complete cds
4316	17655	30643	3.38	7.7E-01	AF189488.1	NT	Colurnix columix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30644	3.38	7.7E-01	AF189488.1	NT	Colurnix columix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32169	1.38	7.7E-01	P16653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	18872	32160	1.39	7.7E-01	P16653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08800.1	EST_HUMAN	y248492.s1 Soares fetal liver spleen (NFLS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087	36689	0.88	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		7.14	7.7E-01	11497821	NT	Archaeoglobus fulgidus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	19399	32748	5.26	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6847	19808	33193	0.66	7.9E-01	P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6900	19509	31601	0.74	7.9E-01	A1253390.1	EST_HUMAN	eq14b12x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
6900	19509	31628	0.74	7.9E-01	A1253390.1	EST_HUMAN	eq14b12x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
7198	20061	33472	0.84	7.9E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.9E-01	AF146783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34824	2.38	7.9E-01	6857752	NT	Mus musculus actinin (Admi-pending), mRNA
8318	21400	34825	2.38	7.9E-01	6857762	NT	Mus musculus actinin (Admi-pending), mRNA
8520	21601	35137	0.53	7.9E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35198	0.53	7.9E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9187	22245	36789	1.33	7.9E-01	6753577	NT	Mus musculus cytochrome P450, 2b8, phenobarbital inducible, type a (Cyp2b8), mRNA
9479	22536	36100	5.24	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536	36101	5.24	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.28	7.9E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11639	24719	38412	2.28	7.9E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24995		2.78	7.9E-01	AL161692.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25157		8.21	7.9E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	28807	1.08	7.9E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7690	20765	34240	0.8	7.9E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	25354		5.2	7.9E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
1154	14318	27372	1.61	7.4E-01	A1598146.1	EST_HUMAN	tr14b08.x1 NC1_CGAP_Bn25-Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2419	15548	28678	0.97	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3820	16980	29883	0.97	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30175	0.71	7.4E-01	AF133310.1	NT	Viral chlamydia phage CTXphi Calcutta-rsR-e (rsR-e) and Calcutta-rsR-b (rsR-b) genes, complete cds
4429	17589	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8027	21110	34628	1.26	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34628	1.26	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21889		1.45	7.4E-01	U87890.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9288	22374	35925	6.88	7.4E-01	BE747503.1	EST_HUMAN	601673026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9357	22432	36890	1.24	7.4E-01	AA187988.1	EST_HUMAN	z667H01.a1 Strategene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:626297 3' similar to SW:TCPO_MOUSE_P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10813	22847	37256	0.7	7.4E-01	11424033	NT	Homo sapiens NY-REN-49 antigen (LOC511133), mRNA
12170	26138		3.69	7.4E-01	6763217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12287	26213		1.7	7.4E-01	A472841.1	EST_HUMAN	1a13h01.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:3043985 3'
4083	17238		0.73	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 67
4738	17873	30866	0.8	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF226421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	18897	33287	6.6	7.3E-01	L36772.1	NT	Mus musculus antigen (CD72) gene
6741	18897	33288	6.6	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	25941	33771	0.93	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7617	20587	34163	0.69	7.3E-01	Z14133.1	NT	D.melanogaster Cnc mRNA for clathrin heavy chain
7718	20782	34268	7.25	7.3E-01	M28511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
7718	20782	34269	7.26	7.3E-01	M28511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
11714	24754	39448	3.29	7.3E-01	AA678018.1	EST_HUMAN	z25508.a1 Soares_fetal_liver_spleen_1INFLS S1 Homo sapiens cDNA clone IMAGE:431769 3'
11714	24754	39449	3.29	7.3E-01	AA678018.1	EST_HUMAN	z25508.a1 Soares_fetal_liver_spleen_1INFLS S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.96	7.2E-01	L28281.1	NT	Rattus norvegicus initiation factor-2 kinase (elf-2a) mRNA, complete cds
2012	15162	28257	3.43	7.2E-01	X79140.1	NT	N.tubacum Nelf-4A13 mRNA
2532	15557	28781	1.96	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	29323	1.27	7.2E-01	AF108100.1	NT	Fowlpox virus, complete genome
3541	16706	29717	2.36	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
3702	16863	29866	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0308 gene, partial cds
3975	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	60203559F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108083.1	NT	Homo sapiens IA-2 gene, intron 18

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4882	18022	31007	2.68	7.2E-01	D80314.1	NT	Lmesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF198778.1	NT	Homo sapiens transcription factor IGF-1M enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel c*
5225	18347	31318	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor IGF-1M enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel c*
5308	18425	31396	0.65	7.2E-01	AL101583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83
7382	20441	33903	0.59	7.2E-01	U89033.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8848	21728	35285	1.31	7.2E-01	AF236091.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241	37437	0.64	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10548	23383	37192	2.25	7.2E-01	BF870061.1	EST_HUMAN	602118381F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4275381 5'
10977	24058	37690	3.26	7.2E-01	U82823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polypeptide precursor (DvA) mRNA, complete cds
12737	25488		4.37	7.2E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
12784	26073		1.46	7.2E-01	Y10168.1	NT	B. thuringiensis PK1 & cap genes, putative
710	13882	28928	11.37	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3130	18306	28320	16.1	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4324	17467	30453	3.07	7.1E-01	7305380	NT	Mus musculus atgadin (Otag), mRNA
4324	17467	30454	3.07	7.1E-01	7305380	NT	Mus musculus atgadin (Otag), mRNA
6089	18251	32578	1.73	7.1E-01	BF881034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6089	18251	32580	1.73	7.1E-01	BF881034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7088	20182	33606	6.48	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyrrolyltryptophan synthase (pr) gene, complete cds
8834	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-408 BT0567 Homo sapiens cDNA
8834	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-408 BT0567 Homo sapiens cDNA
10059	23097	36700	1.6	7.1E-01	BE004405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898468 5'
10821	23655	37286	1.1	7.1E-01	MT2881.1	NT	Human T-cell receptor gamma chain c2 gene
12005	25955		2.04	7.1E-01	AA421492.1	EST_HUMAN	z08h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27479	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15847	28770	1.28	7.0E-01	NE2412.1	EST_HUMAN	yc73e07.s1 Soares_multiple_sclerosis_2Nbl-MSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2621	16847	28771	1.29	7.0E-01	N82412.1	EST_HUMAN	y273e07.s1 Soares_multiple_sclerosis_2Nbt-HMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5189	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	19255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8573	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1635 section 143 of 400 of the complete genome
9517	22952	39150	0.58	7.0E-01	U63888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtdD genes, complete cds
9517	22952	39151	0.58	7.0E-01	U63888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtdD genes, complete cds
11382	24443	39102	1.47	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCH-E04 5'
11382	24443	39103	1.47	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCH-E04 5'
13133	25907	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27585	2.91	6.9E-01	AA593530.1	EST_HUMAN	nm28a08.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	16485	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	16636	29707	16.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465694F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3888943 5'
5902	19091	32405	0.82	6.9E-01	AB035682.1	NT	Branchiostoma belcheri BnNA3 mRNA for notochord actin, complete cds
6112	19292	32627	0.85	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19886	33029	1.12	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3532328 5'
7979	21028	34542	0.59	6.9E-01	AF248963.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21280	34789	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
8168	21280	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
9372	22447		0.86	6.9E-01	AF118048.1	NT	Erioseba dispar cation transporting ATPase (atpase) gene, partial cds
9806	22936	36520	0.58	6.9E-01	AF206319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
9898	22936	36521	0.58	6.9E-01	AF206319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
10619	23653	37263	0.78	6.9E-01	BF242367.1	EST_HUMAN	601880680F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4109419 5'
11538	24592	38268	2.11	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
11538	24592	38269	2.11	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
12146	25949		3.77	6.9E-01	Q89868	SWISSPROT	FORK-HEAD BOX PROTEIN C2 (FORK-HEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFI-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14162	27212	1.94	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2739	15956		1.41	6.8E-01	D80917.1	NT	Synchytrium sp. PCC6803 complete genome, 27/27, 3418552-3573470
2890	14798	27883	1.43	6.8E-01	AA854473.1	EST_HUMAN	q776a06.s1 Soares_papillary_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X59411.1_maf ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4894	17829	30815	1.32	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene: exon III and flanks
4980	18109	31085	0.62	6.8E-01	4758521	NT	Homo sapiens hevin (h-EVIN) mRNA
8838	22878	38460	1.06	6.8E-01	AB037788.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23802		5.72	6.8E-01	AA687638.1	EST_HUMAN	nt13607.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546.1_maf1
11344	24407	38056	2.4	6.8E-01	AJ276575.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38057	2.4	6.8E-01	AJ276575.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11378	24437	38056	1.91	6.8E-01	AF038039.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11378	24437	38057	1.91	6.8E-01	AF038039.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24033	36312	1.57	6.8E-01	AF104151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Anopheles gambiae strain M2 translation initiation factor 4C (4A) (cif-4C) mRNA, complete cds
11806	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial
11806	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial
309	13525	28559	30.38	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13590	28598	26.24	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1861	15104		1.14	6.7E-01	M12132.1	NT	Quail test skeletal muscle tropomyosin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451894.1	EST_HUMAN	zrl2g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2235	16058	28498	5.16	6.7E-01	AF196073.1	NT	Drosophila melanogaster Nts85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	16238	28256	5.81	6.7E-01	6878580	NT	Mus musculus Wislott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30898	0.62	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5828	18820	31894	1.44	6.7E-01	J04836.1	NT	M. berkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6628	18820	31895	1.44	6.7E-01	J04836.1	NT	M. berkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	19286	32984	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	19820	32983	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6453	19820	32984	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6754	19910	33304	0.59	6.7E-01	BE905241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6754	19910	33305	0.59	6.7E-01	BE905241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7488	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7488	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
11198	24265	37900	2.08	6.7E-01	BF354649.1	EST_HUMAN	CM3-H10769-010600-197-c03 H10769 Homo sapiens cDNA
11746	23932	37958	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPII
11959	24944	38949	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48068 Fetal spleen Homo sapiens cDNA 3' and
2570	15685	28819	0.97	6.9E-01	AF076240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2765	15880	28989	1.13	6.9E-01	AF188339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	16743	29760	1.16	6.9E-01	4506880	NT	Homo sapiens aema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sensaphorin) 6A (SEMA5A) mRNA
3748	16909	29913	4.58	6.9E-01	Y07689.1	NT	C. albicans random DNA marker, 282bp
4226	17373		2.48	6.9E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	19829	32990	3.82	6.9E-01	9680577	NT	Mus musculus kinesin light chain 2 (Klcz2), mRNA
7272	20355	33808	0.82	6.9E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33809	0.82	6.9E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7862	20916	34421	3.7	6.9E-01	AV680506.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLCID04 3'
8764	21843	35384	0.58	6.9E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9886	22905		2.34	6.9E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.9E-01	AU118188.1	EST_HUMAN	AU118188 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
640	13825	28948	2.02	6.9E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	28949	2.02	6.9E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3519	19895	28998	5.5	6.9E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30282	1.73	6.9E-01	4504632	NT	Homo sapiens Interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30521	7.71	6.9E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18296	31258	2.88	6.9E-01	U29921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5559	25907	31795	1.86	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
6865	20017	33426	1.3	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
7760	20810	34309	0.74	6.5E-01	X04789.1	NT	Murine Ig-related lambs(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7846	20901	34404	0.59	6.5E-01	AJ789882.1	EST_HUMAN	wc46502.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2321042 3'
10042	23080		0.86	6.5E-01	T78604.1	EST_HUMAN	yc21b04.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23577	37186	2.53	6.5E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10689	23654	37563	2.55	6.5E-01	H67583.1	EST_HUMAN	yr1706.r1 Soares_placenta_8to8weeks_2NbhIP8c-9W Homo sapiens cDNA clone IMAGE:252515 5'
10926	24008	37643	2.08	6.5E-01	AA601267.1	EST_HUMAN	no15c07.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
11030	24109		3.38	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11869	24887	38386	5.43	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit iii, cytochrome c oxidase subunit i, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12566	25386		8.69	6.5E-01	BE465030.1	EST_HUMAN	hm74a10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12840	25689		3.83	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL087c
262	13481	26613	8.59	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dydin light chain mRNA, complete cds
3545	16710	28721	4.42	6.4E-01	U48954.2	NT	Mus musculus dyetroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3964	17122	30126	1.46	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
4614	17751	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
8812	21891	35432	1.58	6.4E-01	AE001247.1	NT	Trponema pallidum section 63 of 87 of the complete genome
10221	23257		0.5	6.4E-01	11418320	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10294	23329	36633	7.31	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10309	23344	36949	1.31	6.4E-01	BF670405.1	EST_HUMAN	602150239F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281128 5'
12693	25461		19.53	6.4E-01	AV75212.1	EST_HUMAN	AV75212 MDS Homo sapiens cDNA clone MDSGCG09 5'
447	19543	26682	3.76	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
548	19741	26765	1.85	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2230	15364	28493	3.29	6.3E-01	U91138.1	NT	Shigella flexneri multi-antigen resistance locus
2646	15769	28684	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2646	15769	28685	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.93	6.3E-01	Y17275.1	NT	Lycopodium obscurum p8a gene, complete CDS
6189	19365	32713	0.84	6.3E-01	BE083908.1	EST_HUMAN	PMD-BT0757-010500-002-005 BT0757 Homo sapiens cDNA
6733	19689	33281	1.01	6.3E-01	L27788.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19689	33282	1.01	6.3E-01	L27788.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21788		3.44	6.3E-01	BE002044.1	EST_HUMAN	601676888F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658351 5'
9087	22166	35712	0.78	6.3E-01	982927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421	22495	36062	0.65	6.3E-01	BF216984.1	EST_HUMAN	601894050F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4102898 5'
9620	22875	36245	3.14	6.3E-01	9827521	NT	Varidola virus, complete genome
9620	22875	36246	3.14	6.3E-01	9827521	NT	Varidola virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 69 of 86 of the complete genome
10641	23675	37285	1.58	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW765395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24378	38024	1.78	6.3E-01	AA877716.1	EST_HUMAN	nt03108.61 NCI_CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:O02816 O02816 HLARK ;
11620	24571	38359	6.18	6.3E-01	A1904160.1	EST_HUMAN	GM-BTD43-060299-046 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11888	24878	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12086	25088	38772	1.47	6.3E-01	6838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9810293	NT	Mus musculus keratin complex 2, gene 5g (Krt2-6g), mRNA
12358	25257		1.6	6.3E-01	AF106227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12682	26029		4.27	6.3E-01	X85528.1	NT	C. limicola pscD gene
5891	18178	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7884	20731		3.59	6.2E-01	AF072253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Carr-r4) mRNA, partial cds
7715	25852	34288	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magee8 gene, Cattractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185
8497	21578	35114	4.67	6.2E-01	HT7286.1	EST_HUMAN	ys01608.61 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lycopodium obscurum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydrogenase-shikimate:NADP ⁺ oxidoreductase gene, complete cds
8648	21091	34606	1.47	6.2E-01	BE562887.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680010 5'
9710	22769		2.56	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10283	23318	35919	6.83	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23481	37087	0.63	6.2E-01	11420783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1), mRNA
10426	23481	37088	0.63	6.2E-01	11420783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1), mRNA
10758	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEINASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10758	23789	37406	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2468	15595		0.27	6.1E-01	6678070	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5653	18847	32129	1.33	6.1E-01	M52940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
7009	20146	33584	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20146	33565	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20263	33736	0.67	6.1E-01	AW105553.1	EST_HUMAN	cd55H03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:U128771_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7254	20337	33787	0.69	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8428	21509	35041	3.47	6.1E-01	AF033535.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8695	22074	35812	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8695	22074	35813	1.51	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9615	22670	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615	22670	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36588	1.05	6.1E-01	AE004462.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
10262	23287	36883	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23868	37489	0.47	6.1E-01	AF026863.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25695		1.16	6.1E-01	X85287.1	NT	M. maris orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
576	13767		4.74	6.0E-01	5802698	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27823	1.83	6.0E-01	AF065263.1	NT	Human respiratory syncytial virus strain CH-89-53b attachment protein (G) gene, complete cds
3917	17076	30073	0.87	6.0E-01	AJ233393.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.26	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5095	18687	31567	1.98	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	UHR-BT-aab-e-10-QUL.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6669	19828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6800	19955	33355	0.86	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW138) (CD138 ANTIGEN)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6855	20268	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6855	20268	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	0.49	6.0E-01	AJ277061.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21307	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21307	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23058	36684	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leucotriene B4 receptor BLT2, leucotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10594	23628		0.61	6.0E-01	BE83778.1	EST_HUMAN	RC2-FN0094-190700-017-c08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38528	2.74	6.0E-01	A1420623.1	EST_HUMAN	ff0807 x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:2085621 3'
12053	25440	32052	2.05	6.0E-01	11421693	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.46	6.0E-01	AA708087.1	EST_HUMAN	z89g05.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12953	25556		1.44	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12958	25683	31768	5.46	6.0E-01	5065303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25980		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14198	27254	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	16518	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	16518	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
							Pharodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
3916	17075	30072	0.82	5.9E-01	U74341.1	NT	Rattus norvegicus casein 2 mRNA, partial cds
4337	17480		3.95	5.9E-01	AF162759.1	NT	Ovis aries SRY gene promoter region
6289	18407	31374	0.66	5.9E-01	AF026568.1	NT	
6654	18754	33140	1.95	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33962	3.08	5.9E-01	AB023488.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7558	20628		0.83	5.9E-01	X88801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34785	0.48	5.9E-01	D80911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719543
8639	21918	35456	0.48	5.9E-01	D12822.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW3/UCx major outer membrane protein (omp1) gene, complete cds
10117	23155		0.84	5.9E-01	P04463	SWISSPROT	E8 PROTEIN
10391	23426	37053	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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10908	23991	37824	2.24	5.9E-01	Q82083	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23989	37832	1.71	5.9E-01	AF187944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AF1837175.1	EST_HUMAN	PM1-DT0041-190700-002-h08 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	AF084628.1	NT	Mus spretus strain SPRET/IEI CD-48 antigen (Cd48) gene, partial cds
12302	26220	32101	1.78	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-lysozin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12798	25633		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1959	16101	28201	1.28	5.9E-01	P40472	SWISSPROT	SM1 PROTEIN
4082	17247	30252	1.11	5.9E-01	BF085738.1	EST_HUMAN	601862474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4637	17773	30753	3.59	5.9E-01	AB006077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4917	18047		2.22	5.9E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Megsld) gene, partial cds, alternatively spliced products
5490	19689		1.02	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5848	18842	32123	0.81	5.9E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.9E-01	D78859.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFijlwara) Homo sapiens cDNA clone GEN-500E08 5'
6442	19609	32972	0.58	5.9E-01	D50801.1	NT	Shigella sonnei DNA for 26 ORF's, complete cds
6862	20265		2.37	5.9E-01	S68091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.9E-01	H41671.1	EST_HUMAN	yrb1603.a1 Soares adult brain N258HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8278	21360	34878	0.66	5.9E-01	AJ280051.1	EST_HUMAN	gbs:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34879	0.66	5.9E-01	AJ280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21469	34991	2.71	5.9E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21469	34992	2.71	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
9092	22171	35716	10.4	5.9E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP98
9172	22260	35763	1.23	5.9E-01	Q27398	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 8-11
9179	22251	35794	0.57	5.9E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9796	22836		0.79	5.9E-01	BF031806.1	EST_HUMAN	PUTATIVE CASEIN KINASE TF-48F2.2 IN CHROMOSOME X
11237	24308	37943	7.26	5.9E-01	AJ248213.1	NT	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11291	24357		3.35	5.9E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 6
11407	24468		1.44	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6756253	NT	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3296	16469	29498	1.48	5.7E-01	Q9WTJ2	SWISSPROT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
							PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	16757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	18662	33014	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3868690 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	z38c06.f1 Soares NIH/MPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Boltyls chirona strain T4 cDNA library under conditions of nitrogen deprivation
7941	20391	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P6CR) (P6C REDUCTASE)
8157	21230		0.55	5.7E-01	AJ251835.1	NT	Mus musculus Kcrq1, Ltscd3, Mash2, Tsc4 and Tsc4 genes, alternative transcripts
10004	23042	36834	1.13	5.7E-01	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36835	1.13	5.7E-01	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37461	0.91	5.7E-01	BF540962.1	EST_HUMAN	60207712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068810 5'
12255	25192		1.28	5.7E-01	BE716051.1	EST_HUMAN	MF3-H10736-180700-003-e02 HT0736 Homo sapiens cDNA
13025	25675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3889	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83133.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601614007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12772	25204	36362					ng75g10.s1 NCI_CGAP_P68 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7
12861	17146	30152	1.39	5.6E-01	AA483535.1	EST_HUMAN	repetitive element;
12880	25460		2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
13167	25753		2.66	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
1238	14397	27459	3.84	5.6E-01	BF73829.1	EST_HUMAN	602132020F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
2766	15931	28880	8.04	5.5E-01	8363912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2768	15981	28901	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2985	16161	29178	6.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
3134	16310	29601	1.17	5.5E-01	H46219.1	EST_HUMAN	PROTEIN P30; NUCLEOPROTEIN P10
3306	16480	29601	1.57	5.5E-01	AF227240.1	NT	Homo sapiens superfamily viral-like activity 2 (S. cerevisiae homolog) (SKIV2L), mRNA
3783	16944	29951	2.83	5.5E-01	AF227240.1	NT	ye18a10.s1 Soares adult brain N256H-B55Y Homo sapiens cDNA clone IMAGE:178288 3'
6249	18370		1.34	5.5E-01	P48755	SWISSPROT	Rabbit oral papillomavirus, complete genome
5288	18388	31356	1	5.5E-01	AF063988.1	NT	FO3-RELATED ANTIGEN-1
			1.01	5.5E-01	U69097.1	NT	Metapneustes sanguinolens entomopoxvirus, complete genome
							Bos taurus MHC class II beta-chain B2A-DIB1 gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase- α , palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase- α , palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
7439	20516		0.74	5.5E-01	AB015598.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8878	21756	36291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HTD458-170200-090-005 HTD458 Homo sapiens cDNA
9889	23008		0.56	5.5E-01	U88415.1	NT	Chinese-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23823	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	ESTD2835 Fetal brain, Stratagene (calf839206) Homo sapiens cDNA clone HFBOQ35
11408	24467	38132	1.64	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	28404	8.11	5.4E-01	7657268	NT	Homo sapiens KIAA0829 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
147	13372	28405	8.11	5.4E-01	7657268	NT	Homo sapiens KIAA0829 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
598	13788	26808	1.01	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1300	14456	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
2328	16461	28894	2.82	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta-carotene dioxygenase (beta-diox gene)
5774	18908	32269	0.89	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19482	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE888592.2	EST_HUMAN	601860278R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806090 3'
7490	20565	34035	1.98	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7490	20565	34036	1.98	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10195	23232		2.69	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243660 5'
11334	24367	38046	2.68	5.4E-01	P38858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11620	24906	38607	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24908	38608	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	A8583398.1	EST_HUMAN	w437g04.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13482 LAMIN A (HUMAN);
529	13722	28748	2.12	5.3E-01	AF010413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heparinase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
2843	15857	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29068	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16488	29506	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4327	17470		1.2	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	A820921.1	EST_HUMAN	zu42h12.y6 Scores ovary tumor NIH-HOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	A820921.1	EST_HUMAN	zu42h12.y6 Scores ovary tumor NIH-HOT Homo sapiens cDNA clone IMAGE:740711 5'
5871	18866	32150	0.95	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Scores NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5871	18866	32151	0.95	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Scores NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE845620.1	EST_HUMAN	7a73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5762	18954	32258	2.32	5.3E-01	BE845620.1	EST_HUMAN	7a73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01850.2	NT	Rattus norvegicus ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
9166	22234	35779	0.78	5.3E-01	BF433956.1	EST_HUMAN	7a71c12.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;
9156	22234	35780	0.78	5.3E-01	BF433956.1	EST_HUMAN	7a71c12.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;
10418	23451	37058	0.65	5.3E-01	A854210.1	EST_HUMAN	w84b02.x1 NCL_CGAP_M415 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
11857	24845	38542	5.63	5.3E-01	BE596281.1	EST_HUMAN	SW/COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
12145	26959		1.73	5.3E-01	AA016053.1	EST_HUMAN	G07338667.1 NIH_MGC_E3 Homo sapiens cDNA clone IMAGE:3682168 5'
839	14017	27072	20.65	5.2E-01	L20770.1	NT	cg30e05.s1 NCL_CGAP_B7 Homo sapiens cDNA clone IMAGE:1441378 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
1190	14352	27410	7.57	5.2E-01	Q8WY30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1216	14379	27438	3.05	5.2E-01	AF224492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 6 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1835	18078		9.88	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment H521C085

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2213	16347	28478	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16364	28369	2.1	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S263 POMP91A and POMP90A precursor, genes, complete cds
3309	16483		1.05	5.2E-01	D73443.1	NT	Acetabacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3401	16558		1.61	5.2E-01	AL116780.1	NT	Bothriopsis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3630	16696	28706	2.01	5.2E-01	AA084185.1	EST_HUMAN	am77605.s1 Stragene schzo brath S11 Homo sapiens cDNA clone IMAGE:161604 3'
3722	16883		0.77	5.2E-01	AF020263.1	NT	Medicago sativa chloroplast melate dehydrogenase precursor (p1mth) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16885	28891	0.87	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xc28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), catractin (CAL-T), NAD(P)H dehydrogenase-like protein (NSDHL), and L2
4729	17684	30846	0.61	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acb), mRNA
5770	16862	32263	0.92	5.2E-01	AA284261.1	EST_HUMAN	zc44d08.T7 Soares, senescent fibroblasts, NblHSF Homo sapiens cDNA clone IMAGE:325168 3'
8932	25862	36562	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9632	25862	36563	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10196	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	zp05b09.r1 Stragene muscle 637209 Homo sapiens cDNA clone IMAGE:628783 5'
10233	23268	36858	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25736		4.83	5.2E-01	P18518	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13617	26941	2.5	5.1E-01	M68509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13651	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt) 16S rRNA gene
665	13651	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt) 16S rRNA gene
1694	14838		1.02	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	AI858485.1	EST_HUMAN	w88b12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427283 3'
4303	17446	30432	2.89	5.1E-01	P66380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE081798.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19622	32879	1	5.1E-01	BE541088.1	EST_HUMAN	6010683006F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6408	19676		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU707 5'
7067	20110	33528	1.36	5.1E-01	R80873.1	EST_HUMAN	y84409.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:146872 3'
8770	21849	35389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 S10023 Homo sapiens cDNA
8770	21849	35390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 S10023 Homo sapiens cDNA
9688	22628	36510	4.65	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9689	22629	36513	3.96	5.1E-01	W22302.1	EST_HUMAN	6581 Human retina cDNA Tap508f-cleaned sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25674		3.49	5.1E-01	BF030207.1	EST_HUMAN	601566883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828787 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12834	26427		1.31	5.1E-01	BF430882.1	EST_HUMAN	nc51110.x1 NCI_CGAP_Bri23 Homo sapiens cDNA clone IMAGE3408218 3' similar to contains element
2203	15338	28464	1.65	5.0E-01	4885552	NT	TAR1 repetitive element;
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.83	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3977	17134	30137	2.67	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19637		0.82	5.0E-01	BF576198.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271839 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M62304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21849	35494	0.68	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043486 3'
9657	21100	34813	2.13	5.0E-01	BF317212.1	EST_HUMAN	601803971F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4196832 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22884	36445	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22884	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10802	23637		1.23	5.0E-01	BE868218.1	EST_HUMAN	601445024F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	25226		3.64	5.0E-01	AF028215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13098	25713		2.26	5.0E-01	AL169302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13991	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13091	27045	1.83	4.9E-01	BF571482.1	EST_HUMAN	602076949F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4249880 5'
1892	14844	27928	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1855	15098	28198	1.34	4.9E-01	U40988.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61654	SWISSPROT	FIBRILLIN 1 PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	16337	32682	2.67	4.8E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	16337	32683	2.67	4.8E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7910	20680	34150	1.61	4.8E-01	AB040061.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20684	34438	0.86	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENTYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYL-TRANSFERASE
7882	20634	34440	0.86	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENTYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYL-TRANSFERASE
9190	22268		1.98	4.8E-01	BF206791.1	EST_HUMAN	601874864F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102903 5'
							hs90-02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907288 3' similar to TR:086714
9389	22484	38028	0.96	4.8E-01	AW339805.1	EST_HUMAN	OB6714 HERC2.
9496	23628		2.2	4.8E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13r1), mRNA
10524	23559	37186	1.05	4.8E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12197	25154		2.61	4.8E-01	AF176912.1	NT	Homo sapiens neurotrophin-1B-cal stimulating factor-3 gene, complete cds
13085	26174		4.94	4.8E-01	AA619582.1	EST_HUMAN	nc22a1.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144852 3'
13094	25714	31639	1.69	4.8E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
13181	25768		1.27	4.8E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
							Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4462	17692		0.69	4.8E-01	4504850	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5624	18918	31892	9.66	4.8E-01	J02987.1	NT	Mus musculus slow skeletal muscle troponin T (Ttnnt) gene, complete cds
6817	19970	39378	0.69	4.8E-01	U92882.1	NT	nu85f09.s1 NCL_CGAP_AW1 Homo sapiens cDNA clone IMAGE:1217513
6827	19960		4.18	4.8E-01	AA656876.1	EST_HUMAN	Homo sapiens reproduction 8 (D6S2289E) mRNA
7459	20544		1.83	4.8E-01	5031650	NT	Homo sapiens chromosome 21 segment HS21C009
7845	20600	34403	1.06	4.8E-01	AL163209.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7838	20688	34497	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7938	20688	34498	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
							yf7710.y5 Soares breast 2NH-Bst Homo sapiens cDNA clone IMAGE:164796 5' similar to contains element
8089	21171	34686	1.91	4.8E-01	AB20744.1	EST_HUMAN	MER8 repetitive element:
8448	22562		1.05	4.8E-01	BE155148.1	EST_HUMAN	FN1-HT0350-201298-004-b04 HT0350 Homo sapiens cDNA
10212	23248		0.55	4.8E-01	BF568833.1	EST_HUMAN	602184287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
10968	24047		1.9	4.8E-01	X83602.1	NT	S. cerevisiae ORFs from chromosome X
12279	25208		1.56	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12509	25918		5.78	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3142	18318		0.59	4.7E-01	AF162387.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
6844	18803	33180	8.07	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086387 5'
7186	20051	33461	0.84	4.7E-01	AL204974.1	EST_HUMAN	qf72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765644 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34662	0.76	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34663	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22562	35804	0.61	4.7E-01	6381501	NT	Rattus norvegicus Spermathe binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate h5N1/997 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41088.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW889448.1	EST_HUMAN	RC3-NT0026-240400-011-E08 NT0026 Homo sapiens cDNA
12401	25281		1.84	4.7E-01	BE687763.1	EST_HUMAN	601511033F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	h411408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'
3837	18997	28868	1.62	4.6E-01	BF693300.1	EST_HUMAN	h411408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5535	18732	31747	0.93	4.6E-01	BF313593.1	EST_HUMAN	602091103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5535	18732	31748	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5588	18763	31828	3.52	4.6E-01	Q90843	SWISSPROT	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5588	18763	31829	3.52	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18867	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5677	18871	32157	3.62	4.6E-01	A247678.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3949337 5'
5677	18871	32158	3.62	4.6E-01	A247678.1	EST_HUMAN	q169h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR-O15338 015338 BUTYROPHILIN;
5685	18979	32169	1.44	4.6E-01	P20080	SWISSPROT	q169h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR-O15338 015338 BUTYROPHILIN;
5763	18955		0.85	4.6E-01	AF212124.1	NT	MEIOSIS SPECIFIC PROTEIN HOR1
5950	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	Arctis schwartzii cyclochrome b gene, partial cds; mitochondrial product
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6908	20221	33849	2.89	4.6E-01	UR2332.1	NT	Methanobacterium thermoautotrophicum from basins 1165761 to 1178238 (section 100 of 148) of the complete genome
6908	20221	33860	2.89	4.6E-01	UR2332.1	NT	Emeria cella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25843	33820	0.66	4.6E-01	L07320.1	NT	Emeria cella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7908	20938	34464	0.78	4.6E-01	AA493377.1	EST_HUMAN	Murine cytomegalovirus p1 protein gene, complete cds
8515	21606	35131	14.55	4.6E-01	BF697389.1	EST_HUMAN	h404405.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943383 similar to contains Alu repetitive element; contains element L1 repetitive element;
8946	22025	35585	0.54	4.6E-01	AA832237.1	EST_HUMAN	602130853F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287628 5'
							co78508.s1 NCI CGAP_Ku65 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:A36941 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	22025	35588	0.54	4.6E-01	AA832287.1	EST_HUMAN	cc76008.st NCL_CGAP_K145 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP- RBOSYLATION FACTOR 4 (HUMAN);
9501	22557	38120	0.03	4.6E-01	P56202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANP-RB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	38121	0.03	4.6E-01	P56202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANP-RB) (GC-B) (GUANYLATE CYCLASE)
9886	22806	36490	0.52	4.6E-01	AF182283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22806	36491	0.52	4.6E-01	AF182283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23218	36809	1.15	4.6E-01	AJ015834.1	EST_HUMAN	wg736f12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10181	23218	36810	1.15	4.6E-01	AJ015834.1	EST_HUMAN	wg736f12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
11238	24307		2.31	4.6E-01	P989103	SWISSPROT	POTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11248	24317	37958	5.03	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37957	5.03	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11780	23946	37573	4.3	4.6E-01	AF018389.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11780	23946	37574	4.3	4.6E-01	AF018389.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	15103	28203	1.15	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2933	16110	29124	4.83	4.5E-01	AA677086.1	EST_HUMAN	455d02.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3380	16552	29565	0.68	4.5E-01	AW083781.1	EST_HUMAN	xc25c08.x1 NCL_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2583290 3' similar to gb:1.07807 DYNAMIN-1 (HUMAN);
3380	16552	29566	0.68	4.5E-01	AW083781.1	EST_HUMAN	xc25c08.x1 NCL_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2583290 3' similar to gb:1.07807 DYNAMIN-1 (HUMAN);
3393	16563	29578	4.48	4.5E-01	Q05783	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3486	16882	29651	1.51	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4139	17291		1.18	4.6E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4186	17356	30329	1.02	4.6E-01	AJ708008.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4292	18478		4.71	4.5E-01	AW873495.1	EST_HUMAN	es086009.x1 Barstead acta HPLR56 Homo sapiens cDNA clone IMAGE:2353480 3'
5058	18186	31161	1.18	4.5E-01	BE963445.2	EST_HUMAN	hc80g02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5698	18880	32145	1.57	4.5E-01	AW608814.1	EST_HUMAN	607657225R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3868023 3'
6740	18896		1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c08 PT0012 Homo sapiens cDNA
7571	20843	34120	0.91	4.5E-01	M37038.1	NT	COAT PROTEIN
							Rat nuclear proteins B23.1 and B23.2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.5E-01	A858849.1	EST_HUMAN	W32e02x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q82823 Q82823
8502	21553		1.11	4.5E-01	M32801.1	NT	SW/USNF COMPLEX 170 KDA SUBUNIT.;
8508	21679	35217	2.87	4.5E-01	A8485398.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							tz5g111x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292844 3'
8758	21835	35376	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
8981	22060		2.36	4.5E-01	11444786	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9200	22278	35817	0.86	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10145	23183		0.96	4.5E-01	96303818	NT	Homo sapiens hypothetical protein DKFZp647G183 (DKFZp647G183), mRNA
10713	23749	37352	25.59	4.5E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10713	23749	37353	25.59	4.5E-01	M86006.1	EST_HUMAN	Bornbyrn nuclear polyhedrosis virus, complete genome
							EST02631 Fetal brain, Striatum (cat#336206) Homo sapiens cDNA clone HFBCY17
							EST02631 Fetal brain, Striatum (cat#336206) Homo sapiens cDNA clone HFBCY17
							join4101.x1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:2703885 3' similar to SW:INT8_MOUSE
11104	24176	37812	2.52	4.5E-01	AW581271.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-8, [1];
11225	24294	37835	2.16	4.5E-01	11430789	NT	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	24586		1.3	4.6E-01	AV718382.1	EST_HUMAN	AV718382 GLC Homo sapiens cDNA clone GLCCE12 5'
12164	28102		5.58	4.5E-01	BE871461.1	EST_HUMAN	G01449201F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE:3852891 5'
12895	25582		1.2	4.5E-01	BF337531.1	EST_HUMAN	G02093275F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4183290 5'
12970	25830		12.42	4.5E-01	11422089	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2094	16294		1.11	4.4E-01	8890503	NT	Mus musculus Integral membrane-associated protein 1 (Itmap1), mRNA
							VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
							FACTOR)
2462	15588	28715	4.18	4.4E-01	P48765	SWISSPROT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	28575	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	28678	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	16595	28680	2.12	4.4E-01	BF056726.1	EST_HUMAN	791402.Y1 NCI_CGAP_B16 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	17482		1.35	4.4E-01	BE378707.1	EST_HUMAN	G01237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609383 5'
5536	18733	31749	1.31	4.4E-01	P04629	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733	31750	1.31	4.4E-01	P04629	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18895	32300	1.58	4.4E-01	S85019.1	NT	muslin (rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 380 nt)
5823	19013	32318	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
							Q82111.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1801125 3' similar to TR:Q29168 Q29168
6074	19256	32584	1.12	4.4E-01	AI08413.1	EST_HUMAN	UNKNOWN PROTEIN;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	19258	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q12zh1.1x1 NCL CGAP_Bir25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q28168 Q28168 UNKNOWN PROTEIN ;
6370	19339	32898	1.07	4.4E-01	AW080785.1	EST_HUMAN	xc27e08.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O05154 O05154 AF1AT0XIN B1-ALDEHYDE REDUCTASE ;
6458	19825		1.05	4.4E-01	AA776132.1	EST_HUMAN	aa5d11.s1 Striatogene scilzo brain S11 Homo sapiens cDNA clone IMAGE:970885 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7657	20329	34104	1.14	4.4E-01	AE090571.1	NT	Helicobacter pylori 26895 section 49 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11678.1	NT	S. tuberculosis mRNA for induced stolon tip protein (partial)
8862	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	z69a03.s1 Striatogene colon (#837204) Homo sapiens cDNA clone IMAGE:508336 3'
8852	22427	35885	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	36023	0.62	4.4E-01	AW812578.1	EST_HUMAN	hh05d08.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW JASH6_HUMAN P62701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10167	23204	36788	1.95	4.4E-01	AL288650.1	EST_HUMAN	q38f09.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10168	23205		2.09	4.4E-01	P36590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337	36942	4.94	4.4E-01	P36590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23820	37228	1.78	4.4E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10585	23820	37227	1.78	4.4E-01	S78404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23882	37486	0.48	4.4E-01	P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24578	38256	1.64	4.4E-01	6691408	NT	Tetrahymena refluxa mitochondrion, complete genome
12435	25308	32087	4.23	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4.4E-01	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
13051	26689		1.41	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13618	26859	2.42	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26860	2.42	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1633	14785	27871	1.11	4.3E-01	AW86580.1	EST_HUMAN	QV4-SN0024-200400-183-601 SN0024 Homo sapiens cDNA
2835	10112		1.34	4.3E-01	AW835289.1	EST_HUMAN	CM4-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3127	16303	28316	0.95	4.3E-01	AW869477.1	EST_HUMAN	MFR-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619	26859	1.27	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4526	13619	26860	1.27	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5071	18189		1.04	4.3E-01	AL101502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
6220	18342		0.94	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
6480	18679	31693	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6480	18679	31694	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6009	19194	92512	1.31	4.3E-01	BE181665.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Samitri ectoderm effector receptor (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Ootumik odumik japonica linG gene
6825	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7598	20658		1.28	4.3E-01	BF348001.1	EST_HUMAN	802023134F1 NCL CGAP_Bum67 Homo sapiens cDNA clone IMAGE:4158298 5'
8022	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
8455	22571	39137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsA gene
8928	22968	39556	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74610.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2888554 5'
8928	22968	39557	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74610.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2888554 5'
10433	23468	37075	0.99	4.3E-01	AW170558.1	EST_HUMAN	xt63405.x1 Soares_NHCc cervical tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to TR-000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.66	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1389	16036	27616	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FISH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA761663.1	EST_HUMAN	nz24403.st NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288686 3'
3687	16858	29882	4.1	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3727	16888	29892	1.09	4.2E-01	AJ280338.1	EST_HUMAN	q94b01.x1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
3803	18477		0.73	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40488
3984	17141	30146	0.74	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
4819	17952	30937	2.57	4.2E-01	AAS4093.1	EST_HUMAN	h98h01.st NCL CGAP_P10 Homo sapiens cDNA clone IMAGE:397777 similar to gb:M33800 HLA CLASS III HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5832	19023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5901	18090	32404	1.63	4.2E-01	AW854182.1	EST_HUMAN	RC3-CT0254-060400-028-g04 CT0254 Homo sapiens cDNA
6334	19505	32883	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7060	20184	33608	8.72	4.2E-01	AJ158472.1	EST_HUMAN	AJ158472 PLAGE2 Homo sapiens cDNA clone PLAGE2000470 3'
7080	20184	33609	8.72	4.2E-01	AJ158472.1	EST_HUMAN	AJ158472 PLAGE2 Homo sapiens cDNA clone PLAGE2000470 3'
7151	25359	33727	3.21	4.2E-01	S82604.1	NT	Brc1-1 breast cancer gene [rat, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7242	20328	33770	8.61	4.2E-01	AL161647.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7745	20805	34294	0.81	4.2E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21264	34788	4.01	4.2E-01	AW857448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8182	21264	34787	4.01	4.2E-01	AW857448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4768038	NT	Homo sapiens cytochrome c oxidase subunit Vic (COX8C), nuclear gene encoding mitochondrial protein, mRNA
9511	22578	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalo virus early phosphoprotein p50 mRNA, complete cds
9511	22578	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalo virus early phosphoprotein p50 mRNA, complete cds
10176	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	295501.s1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10714	23747	37354	1.44	4.2E-01	AW688668.1	EST_HUMAN	MR3-SN0010-280300-103-107 SN0010 Homo sapiens cDNA
11288	24364	39005	1.43	4.2E-01	AB023498.1	NT	Oryzates latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11679	24678	38368	1.87	4.2E-01	BE989485.2	EST_HUMAN	601680352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1118	14283	27338	2.11	4.1E-01	AB05481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1127	14282	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14282	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AB05949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2775	15690	29001	1.46	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3008	16181	29202	2.12	4.1E-01	AL101536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3008	16181	29203	2.12	4.1E-01	AL101536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29561	0.68	4.1E-01	AA906344.1	EST_HUMAN	oj94508.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW981282.1	EST_HUMAN	EST1373384 MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW981282.1	EST_HUMAN	EST1373384 MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4422	17663		0.99	4.1E-01	AA909257.1	EST_HUMAN	om33402.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542818 3'
4789	17824	30912	1.36	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6111	19281	32626	4.84	4.1E-01	BF681383.1	EST_HUMAN	602166800F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6857	20010	33420	0.65	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemodone reinites (Soyes) genes, complete cds
7580	20661	34137	2.48	4.1E-01	U67635.1	NT	Methanococcus Jannaschii section 77 of 150 of the complete genome
8225	21307	34827	1.36	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9282	22868	35918	1.61	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Stipeo-pending), mRNA
9765	22762		0.75	4.1E-01	AF160597.1	NT	Vesaleo gymnoscaudus Vgymf60 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10470	23015		1.56	4.1E-01	AL138076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 348
10622	23856	37266	1.16	4.1E-01	AV849579.1	EST_HUMAN	AV849579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10725	23758	37365	0.68	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10725	23758	37366	0.68	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10806	23839		1.14	4.1E-01	BF349382.1	EST_HUMAN	CN42-HT0137-200989-010-608 HT0137 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	X68700.1	NT	Zea mays-ZmFMS2 gene for 19 kDa zein protein
11675	23903	37525	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12810	26139		2.33	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1084	14229	27286	1.49	4.0E-01	8404858	NT	Laqueus rubellus mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6879258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2061	16053	28316	1.08	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2061	16053	28317	1.08	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2866	13369	26402	1.11	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
3033	16209	28231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	28232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (MIC), Y1D (MID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3788	16947	28955	1.87	4.0E-01	AF068803.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	NADH-FLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4938	18068		8.59	4.0E-01	Q31849	SWISSPROT	EST382891 IMAGE resequencing, MAGK Homo sapiens cDNA
6031	19214	32535	1.07	4.0E-01	AW970610.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6668	19790	33108	0.82	4.0E-01	P27285	SWISSPROT	E2 AND E1; 6 KD PEPTIDE
8113	21195	34714	0.51	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
8201	21263	34806	0.79	4.0E-01	AB018825.1	NT	Homo sapiens OCTN2 gene, complete cds
9208	22286	35827	1.11	4.0E-01	AA323289.1	EST_HUMAN	EST26098 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
11889	24857		1.67	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3828082 5'
12021	25008		2.38	4.0E-01	L76080.1	NT	Synechococcus sp. PCC 9413 transposase gene, complete cds
12463	26978		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
13027	26116		1.38	4.0E-01	Z48301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL029w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	mb84405.1 Scans_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to
13222	25907		1.26	4.0E-01	Z48301.1	NT	SW:NTCR_BOVIN_018875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1;
1408	14563	27638	1.84	3.9E-01	AF206918.1	NT	S. cerevisiae chromosome X reading frame ORF YJL029w
2707	15825	28940	3.34	3.9E-01	AB033019.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2770	15895	28994	5.03	3.9E-01	X82032.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
							H. sapiens B-myb gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2770	15885	28996	6.03	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3166	16341	28949	4.24	3.9E-01	AJ226908.1	NT	Sinorhizobium meliloti egl_syrB2, cysE3 genes and orf3
4180	17340	30333	1.48	3.9E-01	BF592811.1	EST_HUMAN	7B1d01.x1 NCJ_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5106	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601583948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833660 5'
6055	19237	32562	4.58	3.9E-01	BF7206036.1	EST_HUMAN	601862302F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
8410	19578	32940	0.64	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.89	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9062	22141	35686	0.83	3.9E-01	AW177011.1	EST_HUMAN	CN3-CT0105-170889-004-008 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	602018944F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155922 5'
9435	22508	36075	1.73	3.9E-01	AW165888.1	EST_HUMAN	xm8cd04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:084821
9745	22809	36387	1.59	3.9E-01	A1937337.1	EST_HUMAN	004821 KIAA0713 PROTEIN;
10082	23120	36722	2.88	3.9E-01	M19878.1	NT	wp76a02.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFV5_HUMAN P48382 BINDING REGULATORY FACTOR;
10150	23188		0.58	3.9E-01	D86722.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10369	23404	37015	0.92	3.9E-01	D86722.1	NT	Porphyra purpurea mitochondrion, complete genome
10362	23697	37203	0.61	3.9E-01	BF361856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10562	23697	37204	0.61	3.9E-01	BF361856.1	EST_HUMAN	CN2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10836	23869		0.47	3.9E-01	AB037832.1	NT	CN2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11059	24135		1.37	3.9E-01	AV696974.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
12049	25030	38730	1.89	3.9E-01	AV702623.1	EST_HUMAN	AV686974 GK Homo sapiens cDNA clone GKCBQG11 5'
12221	26055		4.03	3.9E-01	AF304354.1	NT	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
12918	26603		1.76	3.9E-01		NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
618	13711		6.1	3.8E-01	AB020291.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1919	15062		1.98	3.8E-01	AE003870.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
2637	15700	28674	1.84	3.8E-01	AF214117.1	NT	Xyella fastidiosa, section 16 of 229 of the complete genome
2687	16059	28801	5.2	3.8E-01	6678002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3068	16242		0.71	3.8E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 6 (Slc1s6), mRNA
3113	16269	28306	1.91	3.8E-01	AF049383.1	NT	Human Immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3572	16737	28752	8.7	3.8E-01	AL181618.2	NT	Plasmodium americanus aminopeptidase N (amprN) gene, partial cds
3628	16762		1.09	3.8E-01	A1807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3843	16702		0.97	3.8E-01	AI807218.1	EST_HUMAN	w38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE164080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30182	0.65	3.8E-01	6754095	NT	Mus musculus general transcription factor II 1 (Gtf2), mRNA
5727	18820	32214	1.11	3.8E-01	Q04688	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	18838		0.63	3.8E-01	S48825.1	NT	p18n protein [mink, Genomic, 2446 nt]
6761	18917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271292-049-e02 BT0537 Homo sapiens cDNA
6899	20214	33844	4.39	3.8E-01	AI374001.1	EST_HUMAN	tas4f11.x1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element
7079	20132	33849	1.38	3.8E-01	AL101613.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7885	20750		4.27	3.8E-01	X61597.1	NT	Mus musculus gene for kallikrein-binding protein
8493	21674	35111	0.64	3.8E-01	JB1385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8764	21833	36373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8826	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22090	35638	1.29	3.8E-01	AL103279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22899		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares_fetal_liver spleen 1NLS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains Alu repetitive element/contains PTR5 repetitive element:
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11699	24696	38398	1.67	3.8E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11824	24813		2.87	3.8E-01	BE19219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11892	24977	38681	2.6	3.8E-01	RA2650.1	EST_HUMAN	yf82h11.s1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11892	24977	38682	2.6	3.8E-01	RA2650.1	EST_HUMAN	yf82h11.s1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12490	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12589	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12895	25463		1.71	3.8E-01	BE382856.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
13105	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31633	1.78	3.8E-01	AF104972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	15678	28759	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29720	10.67	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' and
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares_NSJ_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MP3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30638	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 60 of 206 of the complete genome

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31388	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31388	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	18072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6071	18253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment H921C078
6639	19798	33187	0.7	3.7E-01	M1808.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	18819		0.8	3.7E-01	L10363.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7293	20375	33832	3.48	3.7E-01	115258.43	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7865	21015	34527	0.69	3.7E-01	T68802.1	EST_HUMAN	ye50a07.3 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:66324.5'
8524	21605	35143	1.98	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA020921.1	EST_HUMAN	ok43b11.s1 NCI_CGAP_L42 Homo sapiens cDNA clone IMAGE:1518701.3'
9402	22476		1.34	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10414	23449	37054	4.21	3.7E-01	AI336411.1	EST_HUMAN	q143a07.x1 Scores_fetal_lung_NiHL19W Homo sapiens cDNA clone IMAGE:1950987.3'
10783	23816	37437	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X0568.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37989	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIA00851 gene
11285	24351	37990	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIA00851 gene
11754	23940	37568	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12004	24989		1.42	3.7E-01	AA973640.1	EST_HUMAN	0046d03.s1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:1569221.3' similar to gb:M77698
12066	25047		3.5	3.7E-01	6877878	NT	TRANSSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12137	25654		1.17	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12314	25229		3.94	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	25289		1.82	3.7E-01	D89976.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12821	25548		2.94	3.7E-01	AL121154.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12902	25597	31971	6.99	3.7E-01	Y18000.1	NT	DKFZp782K075.1 782 (synonym: hmsl2) Homo sapiens cDNA clone DKFZp782K075.5'
271	13469	26520	0.77	3.6E-01	AJ009609.1	NT	Homo sapiens NF2 gene
1020	14191		9.07	3.6E-01	U89241.1	NT	Braconia nupae mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human m1p gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	yo03e05.l1 Scores infant brain IN1B Homo sapiens cDNA clone IMAGE:24443.5'
1968	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	yo03e05.l1 Scores infant brain IN1B Homo sapiens cDNA clone IMAGE:24443.5'
1968	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33i02.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2847419.3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	16147	28263	6.7	3.6E-01	AF218207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	16261		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rnagr1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15500		2.8	3.6E-01	X76726.1	NT	P. irregularis (P3804) gene for actin
2556	15931	28808	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181089-011-q07 ST0171 Homo sapiens cDNA
2694	15914	28929	1.89	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE)
2964	18475		8.47	3.6E-01	AF100488.1	NT	ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE
3358	16723	29738	1.98	3.6E-01	X76793.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3558	16723	29739	1.98	3.6E-01	X76798.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4528	17668	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	H. sapiens serotonin transporter gene, exons 9 and 10
4953	17996	30981	0.69	3.6E-01	AJ009609.1	NT	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
5123	18249	31215	3.19	3.6E-01	AW339398.1	EST_HUMAN	Brassica napus mRNA for MAPK alpha2 protein
5209	18330	31302	0.92	3.6E-01	BE067688.1	EST_HUMAN	h02g04.x1 NCI_LGAP_L124 Homo sapiens cDNA clone IMAGE:2872566 3'
5498	18697	31713	0.84	3.6E-01	AJ006565.1	NT	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6211	18388	32735	0.96	3.6E-01	P16431	SWISSPROT	Homo sapiens lps gene intron 5
6807	19767	33155	1.63	3.6E-01	Y10196.1	NT	FORMATE HYDROGENLYASE SUBUNIT 6 PRECURSOR (FHL SUBUNIT 6) (HYDROGENASE-3 COMPONENT E)
7298	20380		3.85	3.6E-01	R94090.1	EST_HUMAN	Homo sapiens PHEX gene
7435	20512	33085	1.52	3.6E-01	AW027174.1	EST_HUMAN	y74a08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:276987 5'
8419	21500	35032	0.76	3.6E-01	P98167	SWISSPROT	w72c10.x1 Soares thymus_NHfTh Homo sapiens cDNA clone IMAGE:2813010 3' similar to TR-O15117
8474	21555	35087	16.45	3.6E-01	AL161583.2	NT	O15117-FYN BINDING PROTEIN, [1]:
							SCO-SPONDIN
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9179	22267	35789	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP173) gene, complete cds
9179	22267	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP173) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8938	22468	38032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8959	22654	38225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
8959	22654	38226	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
8959	22631		0.58	3.6E-01	X02823.1	NT	C. parvovirus p10 gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	35708	18.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y41S
11187	24258	37891	2.42	3.6E-01	BE802390.1	EST_HUMAN	601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915	37540	4.44	3.6E-01	AE000858.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens H1b5 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25297		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12528	25532		1.98	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW190229.1	EST_HUMAN	X00911.1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678116 3' similar to gb:K00568 TUBULIN
13146	25745		1.38	3.6E-01	Z54173.1	NT	ALPHA-1 CHAIN (HUMAN);
214	13437	26467	3.71	3.5E-01	6678833	NT	Pyrococcus sp. pol gene
695	13878	26911	1.03	3.5E-01	AL161581.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
743	13924	26965	1.53	3.5E-01	7709136	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26966	1.53	3.5E-01	7709136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13991	27033	4.88	3.5E-01	BF129786.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
1870	14822	27805	1.28	3.5E-01	U35776.1	NT	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
2871	18088	28808	1.34	3.5E-01	AA223252.1	EST_HUMAN	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
3795	16956		0.73	3.5E-01	BF214381.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:850872 3'
4378	17521	30501	2.62	3.5E-01	AF071253.1	NT	601845470F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4076680 5'
5048	18176	31163	4.34	3.5E-01	M18249.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5323	13349	26378	0.6	3.5E-01	AL161636.2	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5449	18949	31627	1.1	3.5E-01	Q96887	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
5449	18949	31628	1.1	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18861	32146	1.29	3.5E-01	D42046.1	NT	EARLY E2A DNA-BINDING PROTEIN
6367	19537		1	3.6E-01	AW863916.1	EST_HUMAN	Human mRNA for KIAA0086 gene, complete cds
							PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw7903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TRG1068635
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	G1068035 F10F2.1;
6803	19558	33358	0.9	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfide reductase (msrA) mRNA, complete cds
7201	20066		3.38	3.5E-01	X08505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7713	20778	34284	0.59	3.5E-01	P47281	SWISSPROT	S. scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34285	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8265	21347	34882	0.82	3.5E-01	BF368871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8662	21742		0.77	3.5E-01	AF051581.1	NT	RC4-ET0024-280600-014-d07 E10024 Homo sapiens cDNA
9127	22206	35740	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9837	22976	36567	1.75	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10090	23128	36731	4.78	3.5E-01	Z28825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10972	24052	37685	2.62	3.5E-01	X81084.1	NT	X. laevis gene for albumin including HP1 enhancer
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
11810	24800	38469	1.33	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11862	24890	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11980	24995	38667	1.53	3.5E-01	L05145.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12271	26209		1.51	3.5E-01	AF297488.1	NT	yz29J112.r1 Soares_multiple_sclerosis_ZN1-IMPSP Homo sapiens cDNA clone IMAGE:280375 5'
12344	26249		6.66	3.5E-01	X84565.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12507	26348		2.91	3.5E-01	AE001774.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (SBAP48) mRNA, complete cds
12710	26472		1.5	3.5E-01	AE001691.1	NT	B. taurus alpha1 gene for F(0)F(1) ATP synthase alpha-subunit
13106	26026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermoboga maritima section 88 of 136 of the complete genome
13106	26026	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermoboga maritima section 3 of 136 of the complete genome
725	13907		1.78	3.4E-01	AJ242958.1	NT	ys94f11.r1 Soares retina N2b4-R Homo sapiens cDNA clone IMAGE:219597 5'
998	14169	27230	8.2	3.4E-01	Y09788.2	NT	ys94f11.r1 Soares retina N2b4-R Homo sapiens cDNA clone IMAGE:219597 5'
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1357	14512	27895	2.35	3.4E-01	Y00554.1	NT	Pseudomonas fluorescens cdiR, cdiS genes, orf222 and partial inaA gene
2474	15601	28728	2.54	3.4E-01	D90909.1	NT	QV3-HT0261-241189-019-g10 HT0261 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3065	18241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3065	18241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	18302	29403	1.09	3.4E-01	D80809.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNIGC1) mRNA, complete cds
3424	18503	29808	0.78	3.4E-01	AF034802.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylobacterium sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.89	3.4E-01	BF448010.1	EST_HUMAN	7n94601.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR-Q8UJ15
4163	17913		1.48	3.4E-01	AA584198.1	EST_HUMAN	Q8UJ15.DJ18C3.1
4767	17902	30884	1.78	3.4E-01	BE068912.1	EST_HUMAN	nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
5066	18194		4.3	3.4E-01	A1240973.1	EST_HUMAN	MF4-BT0403-230200-262-c01 BT0403 Homo sapiens cDNA
5802	18892	32285	2.64	3.4E-01	AL161694.2	NT	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5932	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02871.1	NT	zn12d11.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6154	19330	32676	0.98	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204503.1	EST_HUMAN	601671811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6364	19634	32883	1.71	3.4E-01	AL120544.1	EST_HUMAN	UH-BH-est-e-12-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718582 3'
6882	20034		1.39	3.4E-01	N95225.1	EST_HUMAN	DKFZp761A249.J1 701 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
7088	20180	33604	1.07	3.4E-01	AA68082.1	EST_HUMAN	zb53er12.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	tm83g06.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb-S37431
8090	21172		0.48	3.4E-01	AE000483.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.68	3.4E-01	Y14930.1	NT	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4246385 5'
8684	21764		1.38	3.4E-01	AA337063.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8760	21839	35380	0.71	3.4E-01	L04690.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
9053	22132	35676	1.87	3.4E-01	P26013	SWISSPROT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	Orbitolus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9621	22676		0.57	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9645	21088	34602	4.68	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
							Ephedra fluviatilis mRNA for PLC-gammaS, complete cds
							Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit -BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9645	21088	34603	4.68	3.4E-01	U19482.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9697	22837	36522	0.86	3.4E-01	U68768.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
10083	23131	36735	2.44	3.4E-01	AJ226084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10695	23728		0.73	3.4E-01	AEO04086.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11267	24336		3.26	3.4E-01	AEO00881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38066	1.86	3.4E-01	AF048981.1	NT	Ruflus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25886.1	NT	Human von Willebrand factor gene, exons 36 and 37
11581	24616	38296	1.91	3.4E-01	M25886.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38476	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-globin/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF061848.1	EST_HUMAN	768412.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:3480846 3'
12110	25090	38793	1.95	3.4E-01	Q27546	SWISSPROT	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (U-NUCLEOSIDE HYDROLASE) (PURINE NUCLEOSIDASE)
12150	25120		2.03	3.4E-01	U63604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12264	25198		1.55	3.4E-01	Z21621.1	NT	Saccharomyces RIB5 gene encoding Riboflavin synthase
12367	25912		1.16	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwifp (cwif) gene, complete cds
12489	25338		10.71	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12517	25944		2.98	3.4E-01	BE218652.1	EST_HUMAN	h42408.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3179127 3' similar to contains PTR5.13
12579	26052		1.79	3.4E-01	8836361	NT	PTR5 repetitive element
12700	25406	32023	1.36	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12954	25160		1.98	3.4E-01	AJ288948.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
19055	25691		2.26	3.4E-01	AF010413.1	NT	Glastridium cellulolyticum partial spoIVB gene and spoOA gene, strain ATCC 35319
15	13253	26253	6.72	3.3E-01	X07890.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
108	13253	26253	3.19	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
650	13636	26863	1.97	3.3E-01	7682485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1227	14387	27450	2.57	3.3E-01	Q12446	SWISSPROT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1335	14492	27562	3.39	3.3E-01	BF566860.1	EST_HUMAN	PROLINE-RICH PROTEIN LAS17
							602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1638	14788	27873	1.26	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1674	14828		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Rss recognition component (Krc), mRNA
1777	14828		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week Homo sapiens cDNA 5' end
2477	15804		6.23	3.3E-01			Homo sapiens uridine monophosphate synthetase (uridine phosphoribosyl transferase and oridine-5'-decarboxylase) (UMPS) mRNA
3014	16190	28216	1.61	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3080	16256		1.09	3.3E-01			INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	28311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3584	16749	29766	1.04	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30068	2.72	3.3E-01	O84845	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30262	1.81	3.3E-01	AF200446.1	NT	Hypocyan fragiforme chitin synthase gene, partial cds
4487	17627		2.37	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for requealidin, partial cds
4812	17945		1.91	3.3E-01	AJ539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57622 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17976	30986	1.02	3.3E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4860	18089	31065	1.14	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 27557/03-26687/68
5439	18339	31617	2.55	3.3E-01	X86819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5439	18339	31618	2.55	3.3E-01	X86819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5907	19096	32411	0.68	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6067	19249	32578	1.37	3.3E-01	BE019650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876753 3'
6067	19249	32577	1.37	3.3E-01	BE019650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876753 3'
6162	19338	32684	1.28	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6832	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter libralis gyrB gene for DNA gyrase B subunit, partial cds
6832	20247	33681	0.59	3.3E-01	AB034233.1	NT	Flexibacter libralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7861	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21638	35379	23.1	3.3E-01	BF683654.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8826	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22390	35941	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9578	22720	36289	1.16	3.3E-01	BE828461.1	EST_HUMAN	OM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9578	22720	36290	1.16	3.3E-01	BE828461.1	EST_HUMAN	OM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	N98866.1	EST_HUMAN	z667h01.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:297849 3'
9752	22630	36260	2.81	3.3E-01	BF378745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG-C) gene, exons 1-3, complete cds
10866	23667	37520	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37675	3.35	3.3E-01	X93963.1	NT	D.mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	X93963.1	NT	D.mauritiana Adh gene
11278	24345		2.1	3.3E-01	BF820499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:42135585 5'
11507	24595	38242	9.35	3.3E-01	BE219351.1	EST_HUMAN	hm51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176878 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11626	24706	38339	3.7	3.3E-01	P47953	SWISSPROT	
12018	25002		2.8	3.3E-01	AA606621.1	EST_HUMAN	cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12036	13253	26253	2.33	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5Jl nodX gene
12250	25190	38357	1.85	3.3E-01	6595319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	26685		22.03	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (277)
488	13694		2.5	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
738	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependant RNA polymerase gene, complete cds
1311	14467	27535	1.48	3.2E-01	Z60202.1	NT	P. vulgaris arc5-1 gene
1421	14576	27648	6.74	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1663	14615		1	3.2E-01	AF020730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28069	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 IMAGE resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 IMAGE resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus P16knf111 1 homeobox (P16knf1), mRNA
2774	15889	29000	1.23	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3898	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.93	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4514	17653	30641	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4821	17758	30740	1.35	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 61.7 KD PROTEIN G13G7.04C IN CHROMOSOME 1 PRECURSOR
4830	17933		0.99	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246805 5'
5398	18588	31560	2.93	3.2E-01	BE173864.1	EST_HUMAN	CM0-H105589-060300-269-f10 H105589 Homo sapiens cDNA
6078	18260	32589	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6433	19601	32965	0.79	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
6729	19895	33277	0.95	3.2E-01	AF016494.1	EST_HUMAN	AV718037 FH1A Homo sapiens cDNA clone FH1AABH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8040	21123	34643	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8365	21446	34969	1.5	3.2E-01	M60286.1	NT	Rat ISO-alpha/natriuretic factor gene, complete cds
8461	21542	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat map NOS-D12Wcat
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21646	35187	14.52	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8656	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8698	21778	35310	0.89	3.2E-01	BF248771.1	EST_HUMAN	601855390F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	35311	0.89	3.2E-01	BF248771.1	EST_HUMAN	601855390F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8871	21950	35485	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8871	21950	35486	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9267	22344	36895	0.97	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9278	22354		2.54	3.2E-01	M88511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10198	23235	36824	4.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.82	3.2E-01	BE328230.1	EST_HUMAN	h39305.x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:3181569 3'
10518	23553		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	TD6813.1	EST_HUMAN	EST04702 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBDZ21
12289	26083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster lentinin A (Lam-A) mRNA, complete cds
12861	25572		3.26	3.2E-01	083217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus Inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25689		2.07	3.2E-01	LS9874.1	NT	Homo sapiens deoxydylate desaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE388576.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618746 5'
							ye90h08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2738	15853	28987	3.39	3.1E-01	R18051.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2762	16001	28985	3.77	3.1E-01	7661871	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2782	16001	28986	3.77	3.1E-01	7661871	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2820	16098		1.28	3.1E-01	AW629038.1	EST_HUMAN	h148h08.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2876391 3'
3242	18416		3.61	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
4016	17173	30181	0.94	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5077	18205	31177	0.7	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5695	18780	31838	9.24	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H11238
5718	18911	32206	0.76	3.1E-01	Z74883.1	NT	Saccharibae chromosome XV reading frame ORF YOL141W
5729	18922		0.83	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5892	19080	32360	2.85	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6595	19755	33141	1.3	3.1E-01	AW963949.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6683	19822	33209	0.96	3.1E-01	AJ284458.1	EST_HUMAN	q39d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874889 3'
6821	19974	33382	0.79	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6805	20220		0.89	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-H05 CT0222 Homo sapiens cDNA
7109	25801	31491	2.32	3.1E-01	BE737982.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7656	20911	34416	0.7	3.1E-01	4985390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	yg4680.1.e1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
10108	23144	36742	0.88	3.1E-01	6879322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10272	23907	36903	1.04	3.1E-01	BF696339.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5'
10272	23907	36903	1.04	3.1E-01	BF696339.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5'
10272	23907	36904	1.04	3.1E-01	BF696339.1	EST_HUMAN	q81e11.x1 NCL_CGAP_K18 Homo sapiens cDNA clone IMAGE:1963980 3' similar to gb:S66700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10334	23989	36979	1.88	3.1E-01	AJ244001.1	EST_HUMAN	yo47h08.e1 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_rna2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10510	23545		0.86	3.1E-01	T65325.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11078	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24533	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	x83g08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24916	38507	2.08	3.1E-01	7682291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24917	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	y89105.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element
12123	25103		1.3	3.1E-01	AF169553.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25288		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304162.1	NT	Silvestratia vitreum 40S ribosomal protein S11 mRNA, partial cds
12613	25412		3.73	3.1E-01	AF169553.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26677		3.82	3.1E-01	AF106779.1	NT	Homo sapiens transcription factor 1GIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
13068	26123		1.22	3.1E-01	10948623	NT	Mus musculus peptidoglycan recognition protein-like (Pglypl-pending), mRNA
74	19579	26336	1.65	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	x83f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1537	14680	27769	5.77	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1638	14984	28094	1.2	3.0E-01	X99082.1	NT	A. limnerius putative gene encoding integrase, Mars2 (RP)
3069	16245		0.8	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	16457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3968	17128	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	FM1-ST0262-261189-001-g01 ST0262 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4836	17772	30762	1.79	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5258	18949	28695	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NFE-ETC) (GATA-3)
5467	18667	31646	6.1	3.0E-01	BE741628.1	EST_HUMAN	601694960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18746	31780	0.64	3.0E-01	AF224696.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF228247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
5621	18815	31863	4.01	3.0E-01	BE669575.1	EST_HUMAN	RC3-BT0333-180700-111-403 BT0333 Homo sapiens cDNA
5621	18815	31864	4.01	3.0E-01	BE669575.1	EST_HUMAN	RC3-BT0333-180700-111-403 BT0333 Homo sapiens cDNA
5658	18952	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129sv Clara cell 10 kd protein (mCC10) gene, complete cds
6670	20198	33624	2.82	3.0E-01	D16813.1	NT	Mouse cycloratin 15 gene, complete cds
6999	18518	31511	0.76	3.0E-01	U02269.1	NT	Strongylocentrotus purpuratus 34167 kDa laminin-binding protein mRNA, partial cds
7065	20118	33592	1.15	3.0E-01	AF228247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20363	33808	0.98	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20558	34028	4.3	3.0E-01	10947007	NT	Mus musculus midkalin (Mkin-pending), mRNA
7670	20738	34214	1.31	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PapA (papA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8568	21649		3.1	3.0E-01	6910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9f), mRNA
8658	21738	35279	0.48	3.0E-01	Z70200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein
8871	21751	35288	1.23	3.0E-01	BE568083.1	EST_HUMAN	601339078F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881884 5'
9029	22108	35849	0.69	3.0E-01	AF141678.1	NT	Streptomyces sulfonolactone isopentadecalin N synthase (pcbC) gene, partial cds
9072	22151		0.82	3.0E-01	7881685	NT	Homo sapiens DKFZP886M0122 protein (DKFZP886M0122), mRNA
9419	22493	36069	1.08	3.0E-01	AF228507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dnmB) gene, complete cds, putative
9773	22613	36391	0.84	3.0E-01	P76389	SWISSPROT	enfrutillate phosphoribosyltransferase gene, partial cds; and unknown gene
9827	22867		0.46	3.0E-01	D80804.1	NT	HYPOPHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 8/27, 630555-781448
10346	23381	36862	0.45	3.0E-01	AF152598.3	NT	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10348	23381	36863	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10606	23640	37248	0.6	3.0E-01	AW118111.1	EST_HUMAN	Xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpaA gene for ER chaperone BIP, complete cds
10629	23663	37271	0.76	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'
10629	23663	37272	0.76	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'
12067	25048	38765	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048	38766	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	PS4680	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.49	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ248885.1	NT	Mus musculus mus proto-oncogene and lgr2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1830	15073	28178	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	16220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex acidus section 68 of 109 of the complete genome
2322	16454	28585	1.01	2.9E-01	AF222718.1	NT	Chrysothrix synovialis mitochondrion, complete genome
3253	16427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3323	18496	28613	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171288-001-112 CT0328 Homo sapiens cDNA
3323	18496	28614	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171288-001-112 CT0328 Homo sapiens cDNA
4003	17160	30169	1.12	2.9E-01	AI610836.1	EST_HUMAN	tp21at1.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	w14d10.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:CS4F8.7 CE15976:
4183	17333	30326	0.61	2.9E-01	AB016426.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4186	17345		0.79	2.9E-01	AW002802.1	EST_HUMAN	w02f10.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2480396 3'
4808	17745	30724	0.98	2.9E-01	AA284488.1	EST_HUMAN	za57d12.r1 NCI_CGAP_GC081 Homo sapiens cDNA clone IMAGE:701691 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4957	18087	31083	0.59	2.9E-01	AB018026.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.99	2.9E-01	AI670898.1	EST_HUMAN	w08003.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.L2 L1 repetitive element;
5320	18087	31063	0.65	2.9E-01	AB018026.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18576		1.59	2.9E-01	R37485.1	EST_HUMAN	y77ef12.s1 Soares infant brain (NIB Homo sapiens cDNA clone IMAGE:28291 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X58098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5884	19073	32382	5.27	2.9E-01	X58098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5907	19085	32397	5.53	2.9E-01	6678662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6181	18357	32705	1.65	2.9E-01	AA418145.1	EST_HUMAN	z097b12.r1 Soares NIH-HMP11_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6411	19580	32841	1.07	2.9E-01	AF797128.1	EST_HUMAN	w027c05.x1 NCI_CGAP_Ju24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.L1 L1 repetitive element;
6455	19322	32886	2.22	2.9E-01	U08420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7126	18552	31468	1.4	2.9E-01	AF142326.1	NT	Mus musculus Filh protein (Filh) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7245	20328	33773	3.11	2.9E-01	C04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7310	20382	33852	1.54	2.9E-01	AF100856.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Birgt (BING1), tapasin (tapasin), RafGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
8104	21186	34705	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34940	0.84	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.84	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	60182570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085113 5'
							Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8534	21615		0.53	2.9E-01	AF197466.1	NT	AL160910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8794	21873	35412	0.82	2.9E-01	AU160910.1	EST_HUMAN	Arabidopsis thaliana sulfuryurea receptor-like protein mRNA, complete cds
9125	22204	35747	1.09	2.9E-01	AF225808.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9233	22311	35853	0.81	2.9E-01	M22452.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9447	22563	36125	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9447	22563	36126	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-B12-ehg-b-02-Q-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2728714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-B12-ehg-b-02-Q-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2728714 3'
11133	24205	37830	1.94	2.9E-01	AJ128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38159	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
							my55h02.s1 NCL_CGAP_PT12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element
11881	24869	38588	2.71	2.9E-01	AA935373.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11888	24874	38571	3.12	2.9E-01	AL139078.2	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							w28805.s1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2588821 3' similar to contains element
12677	25452	32017	1.85	2.9E-01	AW005671.1	EST_HUMAN	MER29 repetitive element
12774	25516		1.89	2.9E-01	V00202.1	NT	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene 1
12777	25519	32001	2.23	2.9E-01	AF092493.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
13125	25734	31944	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13125	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31919	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-1 mRNA, complete cds
582	13774		2.04	2.9E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
587	13778		1.96	2.9E-01	U28145.1	NT	Rattus norvegicus A-kinase anchoring protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.9E-01	AF168050.1	NT	Prune dwarf virus movement protein, complete cds
1308	14462	27528	2.19	2.9E-01	BE313442.1	EST_HUMAN	Guinea guinea oocyte maturation factor Mos (o-mos) gene, partial cds
1308	14462	27530	2.19	2.9E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.9E-01	D86550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
							Human mRNA for setine/threonine protein kinase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1768	14915	28011	1.87	2.8E-01	AW60020.1	EST_HUMAN	QV1-CT0364-120200-065-b06 CT0364 Homo sapiens cDNA
2069	15210	28326	1.49	2.8E-01	AL047820.1	EST_HUMAN	DKFZ58812321_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZ58812321
2200	15335	28462	1.51	2.8E-01	AW611195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812333 3'
2542	15367	28781	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 394 of 400 of the complete genome
2542	15367	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL181585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15948	28939	1.16	2.8E-01	AB020376.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 60kDa heat-shock protein (HSP60) mRNA, partial cds
3038	16212	29234	2.52	2.8E-01	Z14037.1	NT	B. taunus microsatellite (ETH121)
3038	16212	29235	2.52	2.8E-01	Z14037.1	NT	B. taunus microsatellite (ETH121)
3468	16633	28652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 77001-99400 nt. position (47)
4103	17257	30287	1.67	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4240	17386		0.6	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 629 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4582	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF076238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31080	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042801F1 NCI_CGAP_Brim57 Homo sapiens cDNA clone IMAGE:4180129 5'
5008	18135	31109	3.66	2.8E-01	AI272689.1	EST_HUMAN	q159c11.x1 Soares_NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5318	18473	31404	0.61	2.8E-01	X60767.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5426	25804	31602	23.61	2.8E-01	AA349897.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' end
5723	18918	32211	2.67	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
5838	19124		0.93	2.8E-01	AW682583.1	EST_HUMAN	CM1-BN0024-150200-119-g12 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765293.1	EST_HUMAN	oa01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34639 FK606-BINDING PROTEIN (HUMAN);
6059	19241		0.64	2.8E-01	AA404576.1	EST_HUMAN	Z44101.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	20212		0.67	2.8E-01	M36968.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6347	19617	32874	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6347	19617	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-ecf-f04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthomyx heterodurus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7589	20669		1.14	2.8E-01	U05693.1	NT	Martelia quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	A1346126.1	EST_HUMAN	qp48r01.x1 NCL CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8284	21368	34885	1.31	2.8E-01	A1346126.1	EST_HUMAN	qp48r01.x1 NCL CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51698.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	33328	0.6	2.8E-01	AA911629.1	EST_HUMAN	alpha205.s1 NCL CGAP_Co12 Homo sapiens cDNA clone IMAGE:1418683 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8789	21858		7.72	2.8E-01	BF347847.1	EST_HUMAN	602022837.F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158525 5'
9668	22528	36109	1.14	2.8E-01	U17261.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scm-2) gene, complete cds
9912	22952		1.16	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23193	36789				NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10265	23300	36898	0.7	2.8E-01	AF284393.1	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10519	23594		3.8	2.8E-01	7708163	NT	Homo sapiens hypodermal protein (LOC51319), mRNA
10561	23598		1.1	2.8E-01	8028154	NT	Fujinami sarcoma virus, complete genome
10682	24061	37202	0.5	2.8E-01	BE969727.2	EST_HUMAN	601654822.R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639785 3'
10682	24061	37695	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5'
10682	24061	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24080	37727	3.01	2.8E-01	BF696970.1	EST_HUMAN	601862148.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076028 5'
11119	24191	37823				NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11556	24511		1.53	2.8E-01	AF081682.1	NT	602137418.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11851	24840	36533	3.58	2.8E-01	BF974023.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 3/6
11851	24840	36534	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		1.56	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12946	25502	31987	12.79	2.8E-01	D88329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12946	25502	31987	7.61	2.8E-01	BE178698.1	EST_HUMAN	PM4-HT0906-030-400-001-e07 HT0906 Homo sapiens cDNA
12975	25682	31996				EST_HUMAN	601673020.F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:3956598 5'
13052	26098		1.29	2.8E-01	BE900116.1	EST_HUMAN	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
13052	26098		1.59	2.8E-01	11433629	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
489	13883	28717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13813	28835	13.64	2.7E-01	AA450061.1	EST_HUMAN	z33b10.e1 Soares_totid_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:78827 3' similar to contains Alu repetitive element;
1200	14446	27512	2.04	2.7E-01	AB004900.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cde
1850	14803		1.63	2.7E-01	X79815.1	NT	G. lambia SR2 gene
1768	14917	28012	3.16	2.7E-01	W58067.1	EST_HUMAN	zdz2h10.1 Soares_fetal_heart_NbH18W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14988	28059	1.48	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01	AF041575.1	NT	Rattus norvegicus vesicular monocarboxylate transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	AI872772.1	EST_HUMAN	EST175679 Infant brain, Benito Soares Homo sapiens cDNA clone UH101R 5' end
2250	15383	28511	0.94	2.7E-01	AI872772.1	EST_HUMAN	EST175679 Infant brain, Benito Soares Homo sapiens cDNA clone UH101R 5' end
2440	15558	28695	7.07	2.7E-01	Y13968.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2526	15561	28775	4.36	2.7E-01	AI810858.1	EST_HUMAN	tx43011.x2 NCI CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3049	16225		0.98	2.7E-01	BF085284.1	EST_HUMAN	CM1-H10875-080900-385-e05 HT0876 Homo sapiens cDNA
3361	16333	28547	0.68	2.7E-01	8363820	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.94	2.7E-01	AI628015.1	EST_HUMAN	wc92a11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17288	30281	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4133	17288	30282	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.46	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5381	18583	31452	1.98	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA4 (HOXA-1.4)
5907	18902		1.31	2.7E-01	AB033174.1	NT	Astropora myrtillophthalma mitochondrial cyto gene for cytochrome b, partial cds
6472	19839	32898	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6472	19839	32899	0.86	2.7E-01	Q00918	SWISSPROT	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6745	19801	33293	1.05	2.7E-01	AE001094.1	NT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6745	19801	33294	1.05	2.7E-01	AE001094.1	NT	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6918	20233	33667	1.74	2.7E-01	Q61554	SWISSPROT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7197	20062		0.77	2.7E-01	AI540070.1	EST_HUMAN	Archaeoglobus fulgidus section 18 of 172 of the complete genome
7511	20595	34058	0.92	2.7E-01	Q11079	SWISSPROT	FIBRILLIN 1 PRECURSOR
							id08h08.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
							HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7865	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7865	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20938	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7917	20938	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7978	21026	34540	0.86	2.7E-01	L01081.1	NT	Oryzobagus cuticulus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.86	2.7E-01	AA013147.1	EST_HUMAN	z335b11.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
8330	21412	34938	0.56	2.7E-01	AW86503.1	EST_HUMAN	MR1-SN0062-100500-002-409 SN0062 Homo sapiens cDNA
8380	21461	34984	0.80	2.7E-01	R30257.1	EST_HUMAN	ye81k06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8486	21587	35104	0.83	2.7E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8659	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9334	22589	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9334	22589	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9337	22602		2.80	2.7E-01	P37828	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36638	0.8	2.7E-01	D86680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10266	23321	36623	0.9	2.7E-01	AF081848.1	NT	Oryzobagus cuticulus calgranulin C mRNA, partial cds
10323	23398	36968	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23762		0.51	2.7E-01	AB011978.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23768	37418	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23768	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11061	24137						Homo sapiens caveolin-1/-2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11061	24137	37772	2.58	2.7E-01	AJ139269.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12816	25942		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
13034	25681		2.75	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
482	16013	26710	2.8	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
493	13688		1.94	2.6E-01	D16450.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE865087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1468	14822	27705	1.09	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb0440.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M38072.6DS RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cder1 Mouse surfeit locus surfat 3 protein gene (MOUSE);
2159	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	MT1844.1	NT	601126010F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
2811	15735		11.68	2.6E-01	BE272440.1	EST_HUMAN	EST358635 MAGe resources, MAGM Homo sapiens cDNA
3161	16336		1.11	2.6E-01	AW974531.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3871	16834	28845	0.84	2.6E-01	M22342.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3733	16904	28809	1.67	2.6E-01	AF229118.1	NT	EST371580 MAGe resources, MAGF Homo sapiens cDNA
4215	17364	30352	0.79	2.6E-01	AW959510.1	EST_HUMAN	QV1-BT0630-040400-132-c03 B.T0830 Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4478	17618	30597	1.71	2.6E-01	AF175283.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4817	17754	30735	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4817	17754	30736	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4870	17806	30794	1.14	2.6E-01	AA457617.1	EST_HUMAN	sa83d07.f1 Stratagene fetal refseq 937202 Homo sapiens cDNA clone IMAGE:839477 5'
4770	17905	30887	2.26	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhcas3-1) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radicata maturated-like protein (mask) gene, complete cds; chloroplast gene for chloroplast product
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	y51e05.f1 Soares placenta Nb21-F Homo sapiens cDNA clone IMAGE:152288 5'
6165	18277		0.91	2.6E-01	AA894625.1	EST_HUMAN	am33b11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 5'
6457	18657		1.28	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5565	18762	31802	0.97	2.6E-01	M86060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5689	18883		0.84	2.6E-01	AB82398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
							Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plin-2 protooncogene homolog plin-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGIM enhancer 3 genes, partial cds; and unknown gp
5895	19083	32394	0.64	2.6E-01	AF207650.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6196	26211		2.57	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
8330	19501	32859	1.96	2.6E-01	AF582557.1	EST_HUMAN	iso2a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q04289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8330	19501	32860	1.96	2.6E-01	AF582557.1	EST_HUMAN	iso2a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q04289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 8/7
8807	19961	33384	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
8807	19961	33365	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7183	20315	33758	1.04	2.6E-01	AB14380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:U67721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148961.1	EST_HUMAN	CNU-HT0245-031199-085-04 HT0245 Homo sapiens cDNA
7587	25948		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
7828	20686		0.78	2.6E-01	AA196149.1	EST_HUMAN	z082a01.11 Stratiogene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627672 5'
7918	20989	34476	1.73	2.6E-01	R10366.1	EST_HUMAN	y37a03.x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033	21118	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	y82a07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0168-181199-003-412 HT0168 Homo sapiens cDNA
8528	21610	35148	2.97	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150306 5'
8605	21686	36223	1.74	2.6E-01	Q10109	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8832	21971	35506	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.08	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9867	22629	36200	0.92	2.6E-01	X17804.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9940	22879		0.5	2.6E-01	AF057121.1	NT	Lentia canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10072	23110	36714	1.13	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10393	23428		0.63	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10190.1	NT	Homo sapiens PHEX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11816	24804		31.14	2.6E-01	X51765.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	26070		4.14	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	26365	32069	3.86	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.6E-01	D88425.1	NT	Cavia cubana mRNA for serine/threonine kinase, complete cds
13007	25663		1.78	2.6E-01	AE001713.1	NT	Thermoboga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13068	15735		1.43	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
13107	25722		2.04	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.6E-01	U30790.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
261	13472	26503	1.87	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
262	13472	26503	1.7	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
265	13484		2.51	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
856	14032	27093	1.23	2.5E-01	U09964.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapdh-S) gene, complete cds
1086	14251		1.76	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T88637.1	EST_HUMAN	ye11g07.r1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.63	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15008		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2563	15688	28814	1.22	2.5E-01	6679216	NT	Mus musculus protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2565	15690		1.02	2.5E-01	AA251897.1	EST_HUMAN	ze11t12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684882 5'
2702	15820	28936	1	2.5E-01	X95310.1	NT	B.taurus mRNA for D-aspartate oxidase
3489	16666		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385494 IMAGE resequences, MAGM Homo sapiens cDNA
3639	16803	29816	7.18	2.5E-01	AL161617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4438	17678		0.88	2.5E-01	Q03314	SWISSPROT	PHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242491.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6b) gene, complete cds; and Nai3 gene, exons 2-9 and 11-16
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30693	3.69	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4804	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4826	18058		3.54	2.5E-01	AJ230113.1	NT	Mus musculus arnasin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31060	0.8	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4994	18123	31101	0.61	2.5E-01	U93656.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	z35a05.1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:755600 5' similar to gb:M88279
5441	18941	31620	12.21	2.5E-01	S83330.1	NT	P59 PROTEIN (HUMAN);
6080	18282	32591	0.6	2.5E-01	AJ008345.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6081	18283		0.81	2.5E-01	AL163207.2	NT	Homo sapiens KVLQ11 gene
6762	18918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C007
7190	20055	33465	0.64	2.5E-01	6394138	NT	Homo sapiens partial abert-1 gene
7507	20581	34054	0.71	2.5E-01	U13982.1	NT	Rattus norvegicus rab3 (RABIN3), mRNA
7539	20609	34319	1.13	2.5E-01	AF134119.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7770	20828	34365	0.82	2.5E-01	AL161506.2	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7814	20869	34365	4.23	2.5E-01	AL163282.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8028	21111	34630	2.22	2.5E-01	BF106040.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
8039	21122	34642	0.51	2.5E-01	BE980712.1	EST_HUMAN	757a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8421	21502	35034	1.9	2.5E-01	BF038585.1	EST_HUMAN	601653391R2 NIH: MGC 68 Homo sapiens cDNA clone IMAGE:3826198 3'
8591	21672	35210	0.8	2.5E-01	P04482	SWISSPROT	601459238F1 NIH: MGC 68 Homo sapiens cDNA clone IMAGE:3862809 5'
8837	21916	35454	4.07	2.5E-01	H53236.1	EST_HUMAN	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
9076	22155	35600	1.05	2.5E-01	M88828.1	NT	yq44f07.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
9716	22791	36351	16.85	2.5E-01	U89851.2	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9716	22791	36352	16.85	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36339	2.44	2.5E-01	AF085164.1	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36340	2.44	2.5E-01	AF085164.1	NT	Homo sapiens receptor-like kinase LRK10 gene, partial cds
10303	23338	36943	1.31	2.5E-01	AW581597.1	EST_HUMAN	Homo sapiens receptor-like kinase LRK10 gene, partial cds
10560	23685	37183	0.51	2.5E-01	11465952	NT	RC3-STO186-130100-01B-a07 ST0188 Homo sapiens cDNA
10763	23798	37416	1.4	2.5E-01	AW162246.1	EST_HUMAN	Periphrax purpurea chloroplast, complete genome
10767	23800	37422	1.61	2.5E-01	X59491.1	NT	xg40c10.x1 NCJ CGAP LH1 Homo sapiens cDNA clone IMAGE:2830034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
11332	24395	38043	2.96	2.5E-01	D50914.1	NT	Mouse L1M4 LINE DNA
12204	25158	38834	6.16	2.5E-01	AF200528.1	NT	Human mRNA for KIAA0124 gene, partial cds
12233	26167		8.12	2.5E-01	AL161541.2	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.5E-01	AF326363.1	NT	Della brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26763	1.41	2.4E-01	AA930316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 6'
1332	14489	27567	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XTS gene and LZTFL1 gene
1332	14489	27558	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XTS gene and LZTFL1 gene
1415	14589	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1898	15041		26.78	2.4E-01	AF267163.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1949	15092	28183	1.43	2.4E-01	AF251708.1	NT	Zaocys dhumades fructose-1,6-bisphosphatase mRNA, complete cds
2061	15231	28353	1.64	2.4E-01	A1742958.1	EST_HUMAN	wg76405.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:O80267 O80267 KIAA0512 PROTEIN.
2206	15340	28467	1.17	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2336	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36634.1	NT	D. discoideum (Ax3-K) parA gene
2820	16304	29045	2.22	2.4E-01	X71783.1	NT	S. pombe swi6 gene
2846	15930	29069	6.27	2.4E-01	AF030164.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74209.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3956	17016	30016	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17283		0.65	2.4E-01	D29980.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31286	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31287	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
							Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfotransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa
5334	18447	31416	1.89	2.4E-01	U88014.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31416	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	AB025707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5578	18773	31819	0.9	2.4E-01	AB025707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5602	18787	31847	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18904	32266	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5772	18904	32267	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5800	18880		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	26816		0.97	2.4E-01	AJ133898.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
6016	19200	32517	2.54	2.4E-01	BF592338.1	EST_HUMAN	765404.x1 NCL CGAP B-16 Homo sapiens cDNA clone IMAGE:338503 3' similar to SW-SFR4_HUMAN
6106	19286	32620	2.47	2.4E-01	AF035548.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6215	19390	32738	2.49	2.4E-01	7681801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6289	19443	32782	0.94	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6516	19681	33051	0.87	2.4E-01	AA388672.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6665	19824	33212	1.59	2.4E-01	A1698989.1	EST_HUMAN	z170302.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:727683 3'
7498	20573	34046	7.79	2.4E-01	L43001.1	NT	w002311.x1 NCL CGAP_P an1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464
7902	20954	34461	0.69	2.4E-01	AF229944.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
8271	21353	34968	0.5	2.4E-01	X97262.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8271	21353	34968	0.5	2.4E-01	X97262.1	NT	Mus musculus Dxlme48e protein (DXlme48e) mRNA, complete cds
8392	21473	34989	1.48	2.4E-01	AJ006397.1	NT	M.musculus psh gene and promoter
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	M.musculus psh gene and promoter
8544	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Streptococcus pneumoniae m08 and h08 genes; two component system 08
8788	21677	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	Streptococcus pneumoniae m08 and h08 genes; two component system 08
8932	22408	35961	0.58	2.4E-01	AL139077.2	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8932	22408	35962	0.58	2.4E-01	AL139077.2	NT	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106208 5'
9768	22701	36287	0.99	2.4E-01	A1693515.1	EST_HUMAN	Campylobacter jejuni NCTC11108 complete genome; segment 4/6
9805	22945	36530	0.69	2.4E-01	AF220067.1	NT	wd43602.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains
9805	22945	36531	0.69	2.4E-01	AF220067.1	NT	MER22.b1 TAR1 repetitive element;
10694	23688	37287	1.8	2.4E-01	Q03682	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
11006	24085	37722	2.15	2.4E-01	AL161494.2	NT	Drosophila melanogaster SKPB gene, complete cds
11074	24149	37788	1.96	2.4E-01	AF030199.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11447	24508	38174	1.8	2.4E-01	BE296817.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11447	24508	38175	1.8	2.4E-01	BE296817.1	EST_HUMAN	Mus musculus type 1 sigma receptor gene, complete cds
11478	24537		8.04	2.4E-01	Z21647.1	NT	601178415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
12169	26127	38827	1.75	2.4E-01	AF17491.1	NT	601178415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
12289	26932		1.35	2.4E-01	AF004213.1	NT	P. asiatica mosaic virus genomic RNA
12360	26258		1.62	2.4E-01	AJ278191.1	NT	Homo sapiens fragile 18D alpha oxidoreductase (FOR) gene, exon 6
							Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
							Mus musculus mRNA for putative mc7 protein (mc7 gene)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12588	25914		1.95	2.4E-01	V01607.1	NT	Gallus gallus gene coding for a-actin
12639	26151		1.37	2.4E-01	BF228975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13072	25701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BKR gene)
13102	25718		4.16	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13597	26633	1.39	2.3E-01	S75898.1	NT	aromatase [Poaipitula guttata=zebra finches, ovary, mRNA, 3188 nt]
654	13940		6.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
684	13669	26900	29.31	2.3E-01	U57568.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
657	14130	27188	3.67	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1634	14766	27872	1.11	2.3E-01	AJ246480.1	NT	Brassica napus elg gene for S-locus glycoprotein, cultivar T2
1681	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh8 gene, exon 1, partial
2103	16242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2517	15943	28764	1.86	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631015 5'
2717	15535	28945	0.98	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB015033.1	NT	Martellibilia agarivorans gxB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3028	16204	28227	1.08	2.3E-01	AA601379.1	EST_HUMAN	no16d03.s1 NC1_CGAP_Pher1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Abu
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	repetitive element; contains element THIR repetitive element;
3456	16623	29844	1.32	2.3E-01	H69838.1	EST_HUMAN	y121b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
							y97h10.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
							GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic,
3944	17103	30100	0.98	2.3E-01	S82821.1	NT	2212 nt, segment 1 of 3]
4046	17202		5.15	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4470	17610	30688	0.86	2.3E-01	R82252.1	EST_HUMAN	y17101.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4520	17659		1.91	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Synechocystis sp. POC8803 complete genome, 1/27, 1-133859
4811	17748	30728	2.78	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4876	17811	30800	5.65	2.3E-01	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5159	18281	31246	0.87	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5223	18345		1.08	2.3E-01	M16994.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5260	18379	31345	0.63	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5419	18620	31596	2.47	2.3E-01	AB040845.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
							7630608.x1 NC1_CGAP_OY18 Homo sapiens cDNA clone IMAGE:3476889 3' similar to SW:GAG_SMSAY
							P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	SHELL PROTEIN P30; NUCLEOPROTEIN P10];

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6647	18941	32122	5.26	2.3E-01	X06587.1	NT	C. familiaris rom1 gene
6768	18998		0.99	2.3E-01	L39112.1	NT	Vitiforma cornuam unali subunit ribosomal RNA gene
6870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Lactococcus carnosum, Genomic, 2868 nt]
6062	19244	32560	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barsstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6062	19244	32570	1.98	2.3E-01	A1708840.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6784	19949	33348	0.86	2.3E-01	AF198088.1	NT	as27e12.x1 Barsstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7017	20153	33573	4.83	2.3E-01	A1718148.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7260	20343	33796	0.86	2.3E-01	862323.23	NT	Oryctolagus cuniculus cytochrome oxidase subunit Via (cox1a2) mRNA, complete cds; nuclear gene for mitochondrial product
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	as4212.x1 Barsstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element;
7573	20646	34123	2.54	2.3E-01	AF175388.1	NT	Homo sapiens hypodermal protein FLJ20345 (FLJ20345), mRNA
7576	20648	34125	5.37	2.3E-01	AV1719681.1	EST_HUMAN	Secale cereale omega secalin gene, complete cds
7576	20648	34126	5.37	2.3E-01	AV1719681.1	EST_HUMAN	Glycine max resistance protein LM17 precursor RNA, partial cds
7784	20840		4.28	2.3E-01	6754779	NT	AV1719681 GLC Homo sapiens cDNA clone GLCDB308 5'
7789	20845	34338	1.58	2.3E-01	BE888071.1	EST_HUMAN	AV1719681 GLC Homo sapiens cDNA clone GLCDB308 5'
7831	20861		2.8	2.3E-01	N80983.1	EST_HUMAN	AV1719681 GLC Homo sapiens cDNA clone GLCDB308 5'
7968	21018	34530	0.71	2.3E-01	11416821	NT	Mus musculus myosin XV (Myp15), mRNA
7968	21018	34531	0.71	2.3E-01	11416821	NT	601511573F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912869 5'
8036	21118	34637	0.52	2.3E-01	AL161558.2	NT	zai12e08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:282353 5'
8183	21265	34788	1.73	2.3E-01	M69831.1	NT	Homo sapiens protobactherin alpha cluster (LOC83390), mRNA
8690	21770	35300	0.62	2.3E-01	U57999.1	NT	Homo sapiens protobactherin alpha cluster (LOC83390), mRNA
8972	22061	35594	0.58	2.3E-01	AW090541.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
9088	22168	35715	0.52	2.3E-01	AW094460.1	EST_HUMAN	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
9341	22417	35970	0.84	2.3E-01	AA372184.1	EST_HUMAN	Mus musculus prosaparin (psapSGP-1) gene, complete cds
9341	22417	35971	0.84	2.3E-01	AA372184.1	EST_HUMAN	xc50e08.x1 NCI_OGAP_Bim35 Homo sapiens cDNA clone IMAGE:2591554 3'
9780	22820	36398	0.5	2.3E-01	6878318	NT	EST176533 MAGE resequences, MAGH Homo sapiens cDNA
9830	22970	36559	0.53	2.3E-01	BE277880.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X63398)
9885	23024	36616	0.81	2.3E-01	AW084460.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X63398)
10037	23075	36675	1.57	2.3E-01	X52124.1	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3od), mRNA
							601120110F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2966739 5'
							EST176533 MAGE resequences, MAGH Homo sapiens cDNA
							Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

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10071	23109	38712	0.83	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281289-001-104 DT0036 Homo sapiens cDNA
10198	23176	38773	2.62	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	38823	2.48	2.3E-01	AJ293281.1	NT	Rhizobium leguminosarum partial genomic DNA for ectopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10671	23705		5.88	2.3E-01	BF133577.1	EST_HUMAN	601846165R2 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4102082 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11633	24713	38404	2.43	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
12098	25079		1.36	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH101 5'
12281	25210		3.07	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25264		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST144 HT2046 Homo sapiens cDNA clone HCOE44 5'
12395	25873		1.23	2.3E-01	AA080619.1	EST_HUMAN	chr11424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12464	26086						x21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12500	26143	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
12553	26376	31652	7.05	2.3E-01	BE882484.1	EST_HUMAN	601607202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12612	25411		1.77	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12708	25470		2.74	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	25411		1.22	2.3E-01	U46845.1	NT	Plautodes watti distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
13008	25686		1.84	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
82	13327	26355	2.36	2.3E-01	BF475811.1	EST_HUMAN	nec39h12.x1 Lupski_sclafio_nerve Homo sapiens cDNA clone IMAGE:3395650 3' similar to contains element
1698	14749	27833	1.13	2.2E-01	AJ052180.1	EST_HUMAN	MEER38 repetitive element;
2155	15281	28418	2.74	2.2E-01	AF187850.1	EST_HUMAN	alpha14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to
2476	15603	28728	2.19	2.2E-01	M34840.1	NT	TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2654	15777	28890	7.16	2.2E-01	BF677838.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2654	15777	28891	1.63	2.2E-01	BE18258.1	EST_HUMAN	Fresh-water sponge Emr1 alpha collagen (COLF1) gene
2946	16123	29136	1.63	2.2E-01	BE18258.1	EST_HUMAN	602065608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249889 5'
2946	16123	29137	4.94	2.2E-01	BE156625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868180 5'
2946	16123	29137	4.94	2.2E-01	BE156625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868180 5'
2987	16163		2.07	2.2E-01	AF020603.1	NT	PM2-HT0353-281289-003-e12 HT0353 Homo sapiens cDNA
3479	16846		2.35	2.2E-01	AL161562.2	NT	PM2-HT0353-281289-003-e12 HT0353 Homo sapiens cDNA
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

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3848	17008	30009	0.62	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17380	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.6	2.2E-01	U08174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF118102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	0.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4379	17622	30603	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.08	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31058	2.2	2.2E-01	AA211216.1	EST_HUMAN	zfp87c05.1 Stratagene HNT neuron (8837233) Homo sapiens cDNA clone IMAGE:648968 5'
5150	18278		1.57	2.2E-01	L13289.1	NT	Mus musculus vimentin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MF0-HIT0067-201088-002-c10 HIT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5874	19084		3.75	2.2E-01	D64000.1	NT	Synachorysis sp. PCC6803 complete genome, 1927, 23927/29-2538899
6122	19301	32640	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6845	19898	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7166	20290	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7279	20362	33815	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate synthase (pgsa) and ABC transporter ATP-binding protein (etpA) genes, complete cds; and unknown genes
7279	20362	33816	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate synthase (pgsa) and ABC transporter ATP-binding protein (etpA) genes, complete cds; and unknown genes
7442	20510	33991	2.36	2.2E-01	M24138.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24138.1	NT	Human glycophorin B gene, exon 4
7655	20723	34168	0.62	2.2E-01	AE000034.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7678	20830	34436	0.88	2.2E-01	AF287887.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B8 (HOXB8), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7903	20957	34463	0.71	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain: C-125
8210	21292		2.45	2.2E-01	AF155143.1	NT	Mus musculus mm23-M1 gene, promoter region
8280	21362	34881	2.68	2.2E-01	Z49833.1	NT	E.coli sepA and sepB genes
8748	21827	35383	0.61	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds

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9083	22162	35708	0.52	2.2E-01	L28312.1	NT	Mouse HD protein mRNA, complete cds
9087	22176	35720	4.58	2.2E-01	AE001713.1	NT	Thermoboga maritima section 25 of 136 of the complete genome
9117	22196	35740	0.48	2.2E-01	U08984.1	NT	Mus musculus ICR/Swiss glyceraledehyde 3-phosphate dehydrogenase (Gepd-S) gene, complete cds
9224	22302		2.88	2.2E-01	AW855030.1	EST_HUMAN	PM3-CT0263-241288-009-b07 CT0263 Homo sapiens cDNA
9315	22381	35942	1.98	2.2E-01	8383247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Droscophila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF376354.1	EST_HUMAN	MRI-TN0045-110800-008-c02 TN0045 Homo sapiens cDNA
9489	22546	36109	1.42	2.2E-01	W02888.1	EST_HUMAN	z0408.t1 Soares melanocyte 2N4HM Homo sapiens cDNA clone IMAGE:291591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22817	36187	0.76	2.2E-01	AJ008839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9578	22718	36286	4.23	2.2E-01	M89843.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9820	22860	36441	0.65	2.2E-01	Q80980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36854	3.84	2.2E-01	AF197941.1	NT	Furaria hyemalis chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
10159	23198	36792	1.63	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10380	23415	37024	1.11	2.2E-01	9825671	NT	601B69724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 5, complete genome
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y683408.t1 Stratigene ovary (8837217) Homo sapiens cDNA clone IMAGE:76855 5'
							y683408.t1 Stratigene ovary (8837217) Homo sapiens cDNA clone IMAGE:76855 5'
							Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthase A (pqqA) genes, complete cds; and pyrroloquin>
10580	23615	37220	0.6	2.2E-01	AF068264.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10659	23693		0.79	2.2E-01	AF071001.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37345	0.57	2.2E-01	AE001562.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exon 11 and AS
10853	23898	37605	0.48	2.2E-01	AF049720.1	NT	Homo sapiens RNA binding protein MCG310 gene, complete cds, alternatively spliced
11389	24450	38111	1.65	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG310 gene, complete cds, alternatively spliced
11707	24704	38398	5.09	2.2E-01	X01818.1	NT	Drosophila 68C glue gene cluster
11748	23934	37560	3.7	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25181		1.33	2.2E-01	BE870959.1	EST_HUMAN	601446867F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3950670 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathectin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
12319	28156		1.96	2.2E-01	U82671.2	NT	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit -BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	25288		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.80	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
12519	25383		1.47	2.2E-01	AW661822.1	EST_HUMAN	H17502.s1 NCL_CGAP_GJ11 Homo sapiens cDNA clone IMAGE:2972523 3'
13115	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKG Homo sapiens cDNA clone GKCAI-B02 5'
883	14165	27228	1.88	2.1E-01	AA569289.1	EST_HUMAN	nm31et11.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804
988	14167	27228	0.72	2.1E-01	AL161604.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27446	1.45	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1225	14385	27447	1.45	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1540	14682	27771	4.20	2.1E-01	AJ248895.1	NT	Mus musculus mas proto-oncogene and lgt2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1983	15106	28206	2.15	2.1E-01	AA908824.1	EST_HUMAN	cd73602.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518810 3' similar to gbK02765
2224	15358	28488	3.55	2.1E-01	BF68073.1	EST_HUMAN	COMPLEMENT C3-PRECURSOR (HUMAN);
2891	16187	29183	2.52	2.1E-01	6912445	NT	602083128F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247603 5'
3533	16698	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3808	17057		5.61	2.1E-01	9838361	NT	nc90b10.s1 NCL_CGAP_C09 Homo sapiens cDNA clone IMAGE:1166679 3'
4125	17279		0.67	2.1E-01	AE001793.1	NT	Beta vulgaris mitochondrion, complete genome
4165	17315	30310	1.57	2.1E-01	P11675	SWISSPROT	Thermoboga maritima section 105 of 193 of the complete genome
4465	17635	30311	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN E180
4699	17834	30819	1.82	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN E180
4767	17892	30871	0.93	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5138	18261	31228	0.7	2.1E-01	D13567.1	NT	Homo sapiens pap47 gene, complete cds
5416	18618	31562	6.31	2.1E-01	BF672695.1	EST_HUMAN	P. falciparum mRNA for small GTPase rab11
7027	20169	33595	1.05	2.1E-01	AJ223392.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
7038	20691	33508	1.8	2.1E-01	U04642.1	NT	602152001F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4263001 5'
7564	20636	34111	0.77	2.1E-01	Q01859	SWISSPROT	Dodo fragilis mitochondrial 16S rRNA gene, partial
7564	20636	34112	0.77	2.1E-01	Q01858	SWISSPROT	Human olfactory receptor (OR17-2) gene, partial cds
7575	20647		1.88	2.1E-01	AE000972.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7883	20835	34441	1.54	2.1E-01	AF000949.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7930	20980	34488	1.38	2.1E-01	AF088887.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
							Canis familiaris keratin (KR19) gene, complete cds
							Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7630	20980	34489	1.38	2.1E-01	AF068687.1	NT	Glycine max melate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1B), mRNA
							Haemophilus influenzae hmcD, putative haemochromin processing protein (hmcC), putative ABC transporter (hmcB), putative haemochromin structural protein (hmcA), and haemochromin immunity protein (hmcI) genes, complete cds
8700	21780	36313	4.76	2.1E-01	U68398.1	NT	DKFZp434f0614_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434f0614 5'
8897	22078	35615	0.91	2.1E-01	AL040637.1	EST_HUMAN	DKFZp434f0614_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434f0614 5'
8897	22078	35616	0.91	2.1E-01	AL040637.1	EST_HUMAN	Homo sapiens APOL gene, exon 9
9159	22237		0.5	2.1E-01	AB022624.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025W
9237	22314	35856	6.7	2.1E-01	Z36786.1	NT	Yy1e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270854 5'
9704	22763	36323	0.89	2.1E-01	N42536.1	EST_HUMAN	Yy1e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270854 5'
9704	22763	36324	0.86	2.1E-01	N42536.1	EST_HUMAN	A. thaliana mRNA for AIRBP-1b protein
9713	22778	36348	2.72	2.1E-01	X07378.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 9
9817	22857	36437	1.02	2.1E-01	AB036629.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10535	23570	37178	1.31	2.1E-01	Z37087.1	NT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10569	23604	37209	1.97	2.1E-01	P62824	SWISSPROT	(80 KD DIACYLGLYCEROL KINASE)
10578	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11778	24768		1.34	2.1E-01	A1141875.1	EST_HUMAN	q66308.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1881761 3'
11892	24850		1.88	2.1E-01	11036947	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11879	24867	38565	2.6	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10622-040500-013-b11 HT0622 Homo sapiens cDNA
12888	25459		1.92	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12894	25466		1.39	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916675 5'
13158	25763	31828	1.19	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
205	13428	28460	1.92	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
547	13740		1.97	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
717	13869	26937	1.37	2.0E-01	M77086.1	NT	O. carniculus germline IgH heavy chain V-H pseudogene, allotype VH2
833	14011	27067	2.09	2.0E-01	AF027665.1	NT	Mus musculus Major Histocompatibility Locus class II region
1036	14204	27281	1.83	2.0E-01	D90905.1	NT	Synedocystis sp. PCC6803 complete genome, 7/27, 781449-820615
1149	14313	27369	2.81	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1283	14439	27508	1.19	2.0E-01	AJ132895.5	NT	Homo sapiens ract1 gene
1336	14493	27583	1.99	2.0E-01	AW394937.1	EST_HUMAN	PM1-HT0422-281280-002-c08 HT0422 Homo sapiens cDNA
1516	14639	27752	22.4	2.0E-01	4503408	NT	Homo sapiens dystrobrein, alpha (DTNA), mRNA
1582	14734	27816	2.68	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0806

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF280700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.98	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradykinin) gene, complete cds
1755	14804		2.88	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1786	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8822238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Net-D-glucose cotransport regulator gene
2955	16132		0.79	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH85A11
3578	16741	29768	0.72	2.0E-01	P48607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOXLEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.91	2.0E-01	AW238005.1	EST_HUMAN	XP15802.x1 NC1_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740385 3' similar to contains element
3798	16959	20063	0.86	2.0E-01	P34641	SWISSPROT	MER21 repetitive element
3902	16983		0.8	2.0E-01	8680797	NT	GED-11 PROTEIN
4688	17823		8.71	2.0E-01	BE828165.1	EST_HUMAN	Mus musculus bone morphogenetic protein 8 (Bmp8), mRNA
5152	18274	31243	8.41	2.0E-01	8922080	NT	QV4-EN0032-190500-223-603 EN0032 Homo sapiens cDNA
5243	18959	29983	0.8	2.0E-01	P34641	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5561	18758	31797	2.55	2.0E-01	X56600.1	NT	GED-11 PROTEIN
5859	19049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5983	19149	32464	0.82	2.0E-01	X91858.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6303	19476		0.74	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hsfp (HAL5) mRNA, complete cds
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
6659	19816	33208	3.74	2.0E-01	AW360865.1	EST_HUMAN	M. aureus mu class glutathione transferase gene
7445	20522	33985	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141089-001-g08 CT0247 Homo sapiens cDNA
7603	20673	34147	0.83	2.0E-01	P64422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (Pfko) gene, exons 3 through 7
8199	21221		6.16	2.0E-01	AF028026.1	NT	GLYMA-GUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21476	35003	3.12	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8921	22000		0.48	2.0E-01	BE582247.1	EST_HUMAN	M. musculus scp2 gene exon 14
9551	22616	36188	1.17	2.0E-01	U82511.1	NT	M. musculus scp2 gene exon 14
9590	22845	36215	0.62	2.0E-01	U71122.1	NT	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9756	22694		5.42	2.0E-01	AE001278.1	NT	Dictyostellum discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9947	22886	36579	0.52	2.0E-01	P11420	SWISSPROT	Arabidopsis thaliana pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9947	22886	36579	0.52	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10095	23133		2.24	2.0E-01	AF146892.1	NT	DAUGHTERLESS PROTEIN
							DAUGHTERLESS PROTEIN
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF068907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF068907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23406	37016	0.87	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23406	37017	0.87	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23454		0.8	2.0E-01	X78988.1	NT	D.melanogaster DNA mobile element (hoppe)
10616	23650	37259	0.88	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
11078	24154	37781	2.12	2.0E-01	D88088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11078	24154	37782	2.12	2.0E-01	D88088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38597	1.33	2.0E-01		7524759	Chlorella vulgaris chloroplast, complete genome
11908	24895	38598	1.33	2.0E-01		7524759	Chlorella vulgaris chloroplast, complete genome
12668	25443		1.24	2.0E-01	AF206837.2	NT	Pinophytes promeates liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12899	25965		1.04	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12912	25876	31851	1.63	2.0E-01	AW875287.1	EST_HUMAN	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12952	25682	31956	1.63	2.0E-01	A023592.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12977	25636		17.48	2.0E-01	AF078184.2	NT	αB9a10.s1 Soares, testis NIT Homo sapiens cDNA clone IMAGE:1643810 3'
113	13344		4.89	1.9E-01	7548743	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
362	13573	26804	5.99	1.9E-01	AF004353.1	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
673	13859	26889	1.54	1.9E-01	U32581.2	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13869	26890	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
681	13866	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01	7305180	NT	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
1128	14293	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1401	14566	27629	2.42	1.9E-01	AF061282.1	NT	EST677784 Fetal lung II Homo sapiens cDNA 5' end
1486	14620		4.34	1.9E-01	AF184623.1	NT	Sorghum bicolor 22 kDa kafirin cluster
2456	15584	28711	3.86	1.9E-01	8922633	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2968	16165	29181	3.81	1.9E-01	U68068.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
3004	16179		7.53	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16850	29666	4.07	1.9E-01	D13197.1	NT	Stimodon hesperus p53 gene, partial cds
3559	16734	29760	4.94	1.9E-01	R16467.1	EST_HUMAN	Gallus gallus ovalbumin (Y) gene, complete cds
3907	17066	30065	1.09	1.9E-01	AF284017.1	NT	Mouse gene for immunoglobulin diversity region D1
4100	17255	30256	3.86	1.9E-01	AB000784.1	NT	y42f10.t1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:129547 5'
4193	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4251	17397		1.31	1.9E-01	AE001912.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
							CM3-CT0315-271189-045-b11 CT0315 Homo sapiens cDNA
							Deinococcus radiodurans R1 section 49 of 229 of the complete chromosome 1

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4348	17489	30471	0.89	1.9E-01	BE884943.1	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4502	17729	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
6124	18250		1.08	1.9E-01	AF223842.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	X72987.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2610444 3' similar to gb:A75779 RETINOIC
5761	18953	32256	8.03	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
5962	19148	32483	1.08	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6006	19191		2.45	1.9E-01	AU133116.1	EST_HUMAN	Mus musculus Wm protein (Wm) gene, complete cds
6457	19624	32987	1.03	1.9E-01	AU782391.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6518	19883	33054	1.1	1.9E-01	AW149462.1	EST_HUMAN	W154102.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2394089 3'
7112	18538	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	X1408.x1 NCI_CGAP_Kd8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7138	20273	33713	0.74	1.9E-01	AF034920.1	NT	Yg09a12.a1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 3' similar to contains MER13
7409	20487	33957	0.92	1.9E-01	U73946.1	NT	repetitive element;
7638	20707	34186	0.78	1.9E-01	U93688.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7861	20728	34204	1.38	1.9E-01	U90922.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7708	20773	34258	2.64	1.9E-01	AF072724.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
8174	21256	34778	1.83	1.9E-01	AL161557.2	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
8885	21964	35500	13.56	1.9E-01	AB033024.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
9146	22226	35768	1.5	1.9E-01	M14598.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
9146	22225	35769	1.5	1.9E-01	M14598.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	Homo sapiens mRNA for KIAA1198 protein, partial cds
10447	23482	37080	0.81	1.9E-01	BE830353.1	EST_HUMAN	Marsupial cat beta-globin gene mRNA, partial cds
10447	23482	37081	0.81	1.9E-01	BE830353.1	EST_HUMAN	Marsupial cat beta-globin gene mRNA, partial cds
10880	23965	37593	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10992	24071	37704	2.18	1.9E-01	AF223391.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12025	25009	38711	2.21	1.9E-01	A1243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	25028	38735	1.48	1.9E-01	U07344.1	NT	Influenza A/Guangdong/249/72 nucleoprotein (seg 5) gene, 5' end

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	26274	1.85	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
270	16009	26519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Oxy gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	26625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13946	26663	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1003	14176	27235	1.8	1.8E-01	AB12212.1	EST_HUMAN	waf102.x1 NCI_CGAP_L24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmod Dqps, complete genome
1317	14473	27640	6.87	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1633	14686	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1633	14686	27768	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15038		1.91	1.8E-01	AF733708.1	EST_HUMAN	cg22d10.x5 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075836 O75836 GAMMA BUTYROBETAINE HYDROXYLASE;
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Soya6, Soya6, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	16873		3.34	1.8E-01	AW835728.1	EST_HUMAN	QV3-DT0018-081289-038-g04 DT0018 Homo sapiens cDNA
2963	16140		2.3	1.8E-01	AF184589.1	NT	Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds
2968	16144	29163	1.16	1.8E-01	AW182300.1	EST_HUMAN	341a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2669756 3'
3194	16369	29375	1.81	1.8E-01	AW895178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3452	16619	29638	0.77	1.8E-01	BF183582.1	EST_HUMAN	601808723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3712	16873	29877	0.87	1.8E-01	H03369.1	EST_HUMAN	345e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3712	16873	29878	0.87	1.8E-01	H03369.1	EST_HUMAN	345e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4453	17653		0.92	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4678	17813	30801	5.61	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
4895	18026	31011	2.68	1.8E-01	AB051897.1	NT	Mus musculus Soya6, Soya6, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5129	18254	31219	0.85	1.8E-01	X78794.1	NT	N. tabacum mRNA pNA-36
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	MIR3-ST0203-151269-112-g06 ST0203 Homo sapiens cDNA
5208	18327	31297	2.65	1.8E-01	AF181268.1	NT	Mesocricetus auratus Na-tauracholates cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	AF439881.1	EST_HUMAN	1657e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5261	18409	31376	1.2	1.8E-01	Y08310.1	NT	M. boarii mtaC and mtaB genes

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.61	1.8E-01	BE082838.1	EST_HUMAN	RC8-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5829	19115	32428	1.19	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6047	19230	32554	0.95	1.8E-01	N28629.1	EST_HUMAN	W38708.R1 Soares melanocyte 2N14-IM Homo sapiens cDNA clone IMAGE:284063 5'
6256	19430	32778	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6256	19430	32777	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6841	19800	33189	1.16	1.8E-01	Q8QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6688	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	W62702.R1 Soares_multiple_sclerosis_2N14-IMSP Homo sapiens cDNA clone IMAGE:278163 5'
7146	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
7146	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
7202	20067	33477	0.87	1.8E-01	BE961363.1	EST_HUMAN	Citrus limonius mRNA for vsus, complete cds
7604	20674	34148	0.81	1.8E-01	AP001611.1	NT	601648361.R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3832247 3'
8810	21888	35431	0.98	1.8E-01	AW068118.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 5/14
9543	22008	36176	1.58	1.8E-01	M73258.1	NT	EST378181 IMAGE ressequencing, MAGI Homo sapiens cDNA
8574	22716	36284	1.62	1.8E-01	6626232	NT	Human cellular DNA/Human papillomavirus proviral DNA
9882	22741		0.6	1.8E-01	AA469761.1	EST_HUMAN	Bacteriophage like, complete genome
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	ri02a05.61 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element;
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	S. commone orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S. commone orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9881	23020	36813	0.91	1.8E-01	P06123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9886	23025	36817	0.71	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.46	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10785	23818	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0589 protein, partial cds
10873	23958	37698	2.02	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10917	24000	37633	5	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, hsdR and hsdS genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
10975	24054	37698	4.41	1.8E-01	AF019107.1	NT	Dicotyledon discoidium unknown (DG1041) gene, complete cds
11270	24338	37976	2.06	1.8E-01	M69267.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24608	38284	1.41	1.8E-01	AW275728.1	EST_HUMAN	xp40h10.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742883 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23636	37663	8.94	1.8E-01	X57033.1	NT	B. laurus mRNA for potassium channel
12061	25042	38751	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thrombospondin receptor (Tbr22), mRNA
12124	25104	38808	1.77	1.8E-01	AA085094.1	EST_HUMAN	cp2798.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.26	1.8E-01	BF348623.1	EST_HUMAN	6020718928F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4155318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	26541		3.28	1.8E-01	Q98882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)
12942	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	YH4810.r1 Soares placenta Nib2-P Homo sapiens cDNA clone IMAGE:133027 5'
12988	25643		4.98	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hck1)
13035	26134	31548	1.7	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcohe), mRNA
591	13782	26801	6.4	1.7E-01	BE385164.1	EST_HUMAN	601274504F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3615768 5'
828	14006	27063	3.16	1.7E-01	X53330.1	NT	P. humani Histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.79	1.7E-01	P38616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1083	14249	27305	0.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1083	14249	27308	0.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1800	15008	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2038	15179		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2822	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VBCO gene, partial cds
2822	16100	29113	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VBCO gene, partial cds
2883	16169	29186	1.47	1.7E-01	AA336608.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3061	16237	29257	1.09	1.7E-01	AJ238738.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3061	16237	29258	1.09	1.7E-01	AJ238738.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3174	16349	29356	1.65	1.7E-01	AF081514.1	NT	Taus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16818	29637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16930	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17203	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/ITK gene fused to intron 5 of the AF-4/TEL gene
4681	17816		2.49	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4884	18014	30698	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4981	18080	31068	1.31	1.7E-01	A1247635.1	EST_HUMAN	cf157a08.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to coronins OFR.b1 OFR repetitive element:
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	001557250F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5312	18428	31389	0.81	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MBP1 (C-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470688.1	EST_HUMAN	nef3a02.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470688.1	EST_HUMAN	nef3a02.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18803	32188	0.82	1.7E-01	U43599.1	NT	Brugia pahangi microfilament protein SHP3 (shp3) gene, complete cds
6459	19828	32888	12.64	1.7E-01	H727118.1	EST_HUMAN	ys02g06.s1 Scores_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:213658 3'
6517	19882	33052	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta28c11.x1 Scores_fetal_lung_NHL19W_Homo sapiens cDNA clone IMAGE:2045492 3'
6517	19882	33053	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta28c11.x1 Scores_fetal_lung_NHL19W_Homo sapiens cDNA clone IMAGE:2045492 3'
6892	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	60094406771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980248 3'
7019	20155		1.94	1.7E-01	AF026562.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7140	20275		0.69	1.7E-01	Z92810.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20525	33938	8.61	1.7E-01	BE794179.1	EST_HUMAN	601669022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7666	25850	34208	0.64	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8045	21128	34648	1.28	1.7E-01	AF000573.1	NT	Homo sapiens homocysteine 1,2-dioxygenase gene, complete cds
8150	21232	34782	0.75	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8472	21553	35063	7.35	1.7E-01	7709426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21553	35064	7.35	1.7E-01	7709426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8895	21974	35511	0.5	1.7E-01	AW982873.1	EST_HUMAN	RC2-BN0032-120200-011-rt10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.83	1.7E-01	D00394.1	NT	Rat (SHR strain) SX1 gene
9045	22124	35668	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neurotrophin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neurotrophin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.91	1.7E-01	RT7002.1	EST_HUMAN	yf68g02.r1 Scores_placenta_Nb2HP_Homo sapiens cDNA clone IMAGE:144242 5'
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22828	36407	9.03	1.7E-01	AP0071608.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389584 IMAGE resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389584 IMAGE resequences, MAGO Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8816	22855	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
8882	23031	36821	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9892	23031	36822	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36845	0.93	1.7E-01	AJ251748.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Human septins chromosome 21 segment HS21C084
10605	23639	37247	1.56	1.7E-01	11427203	NT	Human septins solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10607	23841	37249	1.66	1.7E-01	AA627972.1	EST_HUMAN	hcg0e07.s1 NCI_CGAP_Co8 Homo septins cDNA clone IMAGE:1148282 3' similar to gb1.25081 TRANSFORMING PROTEIN RHOC (HUMAN);
10819	24022	37636	9.54	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo septins cDNA clone IMAGE:3613258 5'
11045	24122	37768	2.12	1.7E-01	AA814617.1	EST_HUMAN	α43a03.s1 NCI_CGAP_CNS1 Homo septins cDNA clone IMAGE:1428624 3'
11373	24434	38090	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11373	24434	38091	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24736	38427	1.71	1.7E-01	AA883375.1	EST_HUMAN	α45f09.s1 Scores_NFL_T_GBC_S1 Homo septins cDNA clone IMAGE:1460297 3'
12011	24996		1.5	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.97	1.7E-01	P65899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.97	1.7E-01	P65899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11416157	NT	Homo septins calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo septins chromosome 21 segment HS21C078
12567	25920		1.18	1.7E-01	AB24404.1	EST_HUMAN	hcg05x1 NCI_CGAP_U11 Homo septins cDNA clone IMAGE:2274872 3' similar to gbM73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12507	25600	31972	7.24	1.7E-01	U01917.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo septins mevalonate kinase gene, exon 6 and 7
697	15935	26913	1.16	1.6E-01	F31497.1	EST_HUMAN	y176f12.1 Scores placenta Nb2HP Homo septins cDNA clone IMAGE:135568 5'
1651	14703	27783	4.25	1.6E-01	AF208117.1	NT	Homo septins homeobox protein OTX2 gene, complete cds
1810	15053		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Macdfr E, complete genome, segment 3/4
1877	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Craesosthea gigas RNA polymerase II largest subunit mRNA, partial cds
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2562	16687	28813	2.73	1.6E-01	AB037729.1	NT	Homo septins mRNA for KIAA1308 protein, partial cds
2957	16134	29149	14.1	1.6E-01	AF185589.1	NT	Homo septins cytochrome P450 3A4 (CYP3A4) gene, promoter region
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	Homo septins cytochrome P450 3A4 (CYP3A4) gene, promoter region

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	28889	1.23	1.0E-01	AJ003165.1	NT	<i>Populus trichocarpa</i> cv. Trichobel ABR3 gene
3723	16884	28890	1.23	1.0E-01	AJ003165.1	NT	<i>Populus trichocarpa</i> cv. Trichobel ABR3 gene
3872	17031	30030	0.82	1.0E-01	AE000982.1	NT	<i>Archaeoglobus fulgidus</i> section 145 of 172 of the complete genome
4107	17261		2.8	1.0E-01	AE004413.1	NT	<i>Vibrio cholerae</i> chromosome II, section 70 of 93 of the complete chromosome
4144	17286	30288	1.21	1.0E-01	AF084458.1	NT	<i>Citridia fasciculata</i> typhedoxin I (hml) gene, complete cds
4448	17688	30569	10.91	1.0E-01	AF170680.1	NT	<i>Homo sapiens</i> apelin gene, complete cds
4578	17715		2.49	1.0E-01	AW988901.1	EST_HUMAN	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
4596	17723		4.39	1.0E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Ccp3), mRNA
5060	18188	31182	1.39	1.0E-01	AA088343.1	EST_HUMAN	z84109.s1 Stratiogene colon (8237204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5083	18211	31183	1.8	1.0E-01	AJ006359.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5083	18211	31184	1.8	1.0E-01	AJ006359.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5345	18458		0.93	1.0E-01	AF045283.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.0E-01	L40608.1	NT	Gallus gallus smooth muscle/muscle myosin light chain kinase gene, exon 29
5639	18833	31909	2.9	1.0E-01	AW197498.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31910	2.9	1.0E-01	AW197498.1	EST_HUMAN	xm43101.xt NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2888689 3' similar to TR:O75984 O75984
5651	18845	32126	1.89	1.0E-01	AF034718.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6152	19328	32874	0.73	1.0E-01	BE925603.1	EST_HUMAN	xm43101.xt NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2888689 3' similar to TR:O75984 O75984
6558	19720	33087	2.06	1.0E-01	AL161588.2	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6558	19720	33087	2.06	1.0E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cabe) gene, complete cds
6939	20262	33888	0.79	1.0E-01	AB046788.1	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6985	20213		0.88	1.0E-01	BF883630.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7103	18530	31485	4.15	1.0E-01	AW281215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7481	20628	34001	0.71	1.0E-01	Z49832.1	NT	Homo sapiens mRNA for KIAA1596 protein, partial cds
7955	21005	34518	1.83	1.0E-01	AW248359.1	EST_HUMAN	602130855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4901004 5'
7982	21031	34544	0.84	1.0E-01	6753237	NT	U14-B12-egl-b-08-0-J1.61 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7988	21036		1.03	1.0E-01	AU136525.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR132w
8053	21196	34667	1.82	1.0E-01	L48348.1	NT	2822248.6ptm NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8215	21297		0.53	1.0E-01	BE244087.1	EST_HUMAN	Mus musculus Ca ²⁺ -dependent activator protein for secretion (Cadps), mRNA
8310	21392	34916	0.77	1.0E-01	U38243.1	NT	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004488 5'
							Corilla gorilla androgen receptor gene, partial exon
							TCBAP-E0007 Pediatric pro-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0007
							Bacteroides vulgatus beta-lactamase (cba) gene, complete cds and mobilization protein (mobA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21912	35450	1.08	1.6E-01	Z89119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
9028	22105	35646	0.77	1.6E-01	R13673.1	EST_HUMAN	Y80Y08.J1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:28873 5'
9133	22212		0.74	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35702	1.85	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
9311	22387		0.78	1.6E-01	AF11167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22881		1.77	1.6E-01	BF37517.1	EST_HUMAN	RC3-ST0200-041189-011-h01 ST0200 Homo sapiens cDNA
9854	22894	36475	1.98	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
9891	22931		1.19	1.6E-01	BE156684.1	EST_HUMAN	PM2-H10353-270100-004-f11 H10353 Homo sapiens cDNA
10828	23859	37482	0.5	1.6E-01	11128016	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37609	2.34	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37851	1.94	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37852	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37858	1.62	1.6E-01	BE259649.1	EST_HUMAN	601145783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24498		3.8	1.6E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24694	38388	7.53	1.6E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12277	25207	38363	3.89	1.6E-01	AV719586.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12597	26402	32043	2	1.6E-01	L14933.1	NT	Rat conversase PC8 mRNA, 5' end
12630	25423		1.38	1.6E-01	AW639711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12733	25893		11.84	1.6E-01	AB045310.1	NT	Gucunis sativus KS mRNA for ent-kaurene synthase, complete cds
12833	25816		2.71	1.6E-01	AK024406.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13028	25678		5.04	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25690	31884	1.69	1.6E-01	9606522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13060	25694		1.4	1.6E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3345038 5'
13189	25782		1.29	1.6E-01	BF672696.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
258	13477	26508	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-H10616-040700-197-E05 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-H10616-040700-197-E05 HT0619 Homo sapiens cDNA
600	15984		2.5	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DGA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21G084
1116	14281	27337	1.44	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1121	14286	27341	2.7	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.5E-01	AW195516.1	EST_HUMAN	X1304111.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2896085 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27528	3.22	1.5E-01	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1511	14684	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1857	15100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H-B13-akb-b-09-0-UJ.s1 NCL CGAP_Sub61 Homo sapiens cDNA clone IMAGE:2733941 3'
2980	16166		0.9	1.5E-01	AW572516.1	EST_HUMAN	xw55aa02.y2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:U55072_mart
3100	16276	28290	0.91	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16294	28308	0.82	1.5E-01	O78887	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3433	16801	29820	5.78	1.5E-01	AA635049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3454	16821	29841	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3454	16821	29842	0.73	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3851	17011	30011	2.35	1.5E-01	U09364.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3887	17028	30025	0.83	1.5E-01	7108388	NT	Mus musculus [CR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3881	17040	30037	0.77	1.5E-01	M97982.1	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3970	17128	30131	2.45	1.5E-01	AW685983.1	EST_HUMAN	XYNA: Thermotoga bacterium; xynA; 4182 base-pairs
3987	17144	30149	0.88	1.5E-01	AJ003165.1	NT	h10006.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3987	17144	30150	0.88	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4161	17312	30308	1.16	1.5E-01	AW368659.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
4210	17359	30348	0.67	1.5E-01	Z12823.1	NT	RC2.H10149.101099-012-c09 H10149 Homo sapiens cDNA
4289	17442	30428	0.85	1.5E-01	AL163284.2	NT	B. napus mitochondrion DNA for ORF158
4847	17980	30989	1.64	1.5E-01	BF687885.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4874	18891	29002	2.33	1.5E-01	BF685381.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4088223 5'
5114	18242	31207	1.5	1.5E-01	AL161560.2	NT	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5370	18573	31441	1.91	1.5E-01	P07998	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5399	18601	31571	1.33	1.5E-01	AF256562.1	NT	THROMBOSPONDIN 1 PRECURSOR
5443	18843		5.95	1.5E-01	P15198	SWISSPROT	Caiman crocodilus MHC class II beta chain (hclbeta) gene, complete cds
6655	18849	32131	4.8	1.5E-01	AW850754.1	EST_HUMAN	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
6897	18891	32182	6.66	1.5E-01	U65016.1	NT	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
6897	18891	32183	6.66	1.5E-01	U65016.1	NT	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
6029	19212	32532	0.82	1.5E-01	4508810	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
						NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
						NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
						NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN8A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32847	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6128	19307	32848	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6168	19344	32890	2.19	1.5E-01	AJ270505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19406	32862	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.98	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L), mRNA
6474	19641	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6631	25828	33178	3.68	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6661	19820	33207	4.73	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6672	19831	33220	1.67	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28482	SWISSPROT	AMELOGENIN
6823	19976	33383	0.86	1.5E-01	AA714760.1	EST_HUMAN	mw30410.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241871 3'
6852	20006	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31500	6	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE resequencing, MAGK Homo sapiens cDNA
7158	25840		0.8	1.5E-01	AA811545.1	EST_HUMAN	cb73802.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element;
7366	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20822	34089	1.63	1.5E-01	AB79157.1	EST_HUMAN	wf5208.s1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775	20832	34322	1.68	1.5E-01	AW500811.1	EST_HUMAN	UHF-BNO-akt-3-05-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7775	20832	34323	1.68	1.5E-01	AW500811.1	EST_HUMAN	UHF-BNO-akt-3-05-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7919	20970	34477	0.79	1.5E-01	U46660.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of bcs1-1 (SOL3) gene, complete cds
8248	21330	34946	0.89	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21495	35028	1.1	1.5E-01	AA970317.1	EST_HUMAN	0085g12.s1 NCI_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M28082
8507	21588		1.06	1.5E-01	BE884789.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8594	21675		14.14	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.5E-01	L27835.1	NT	C16800 Cortech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-329H-09 5'
8793	21872	35411	2.17	1.5E-01	D84478.1	NT	Panglossinadon glycosyl growth hormone (GH) mRNA, complete cds
8814	21893		0.79	1.5E-01	P43448	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9038	22117	35680	3.12	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
							Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8805	22381	35932	2.58	1.5E-01	N74228.1	EST_HUMAN	zsf59a06.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:286868 3' similar to
9394	22469	36033	1.34	1.5E-01	BF585465.1	EST_HUMAN	PIR:944443 S44443 RAD23 protein homolog2 - human;
9401	22475		2.52	1.5E-01	AF754819.1	EST_HUMAN	GVO00404 Human Pteridase Differential Display Homo sapiens cDNA
9605	22680		0.84	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPA4HB12 5'
9652	21095	34809	6.7	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
							Adiponectin transmembrane vitellogenin mRNA, partial cds
10022	23060	36856	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10126	23163	36761	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10126	23163	36762	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.5E-01	X98852.1	NT	P. tentaculus mRNA for integrin beta subunit
10495	23530		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37161	2.38	1.5E-01	A1814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27508 BETA
10516	23551	37162	2.38	1.5E-01	A1814046.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10568	23633	37242	1.22	1.5E-01	U40832.1	NT	wk53h12.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10761	23794	37413	1.69	1.5E-01	AJ011904.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10761	23794	37414	1.69	1.5E-01	AJ011904.1	NT	Dentio retro transcription factor Pax9b (Pax9) mRNA, complete cds
10835	24017	37649	1.67	1.5E-01	BE088492.1	EST_HUMAN	Claviceps purpurea ps1 gene
10936	24017	37650	1.67	1.5E-01	BE088492.1	EST_HUMAN	Claviceps purpurea ps1 gene
11063	24139	37773	4.46	1.5E-01	AL163280.2	NT	CM2-BT00688-210300-122-f11 BT00688 Homo sapiens cDNA
11063	24139	37774	4.46	1.5E-01	AL163280.2	NT	CM2-BT00688-210300-122-f11 BT00688 Homo sapiens cDNA
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
11925	24911		1.34	1.5E-01	A1183704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12232	25953		38.98	1.5E-01	BF700582.1	EST_HUMAN	IL5-CN0024-030300-026-D04 CN0024 Homo sapiens cDNA
12628	25422		1.64	1.5E-01	AF030358.2	NT	qe72a01.x1 Soares fetal lung NBH-19W Homo sapiens cDNA clone IMAGE:1744636 3' similar to
12633	25423		1.23	1.5E-01	AJ298332.1	NT	gb:M17987 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12698	25876		0.64	1.5E-01	R83077.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12749	25468		1.52	1.5E-01	AP001514.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12778	25520	32002	1.41	1.5E-01	9695473	NT	Mus musculus mRNA for death inducer-collagenase-1 (Die-1)
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	yp87e04.l1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
12832	25898	31857	7.68	1.5E-01	AL138074.2	NT	Bacillus halodurans genomic DNA, section 8/14
							Lymphocystis disease virus 1, complete genome
							AV741272 CB Homo sapiens cDNA clone CBDAAGD04 5'
							Campylobacter jejuni NCTC11168 complete genome, segment 1/6

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13183	25789	31832	6.61	1.6E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	26138		2.26	1.6E-01	9631294	NT	Melanoplus sanguipes entomopoxvirus, complete genome
310	13526		1.23	1.4E-01	AF008663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S6P to TCRBV21S2A2 region
633	14108		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1288	14444		2.98	1.4E-01	T81984.1	EST_HUMAN	yt54c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.48	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermoplasma maritima section 22 of 136 of the complete genome
1954	15037		1.27	1.4E-01	AW136741.1	EST_HUMAN	UHH-B1-act-a-08-0-UJ.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714008 3'
2042	15183		14.84	1.4E-01	AA720615.1	EST_HUMAN	iy72807.s1 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:1283821 3'
2544	15669	28783	1.02	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2853	15967	29077	3.34	1.4E-01	AB33496.1	EST_HUMAN	wm74d01.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4289	17434	30421	9.45	1.4E-01	AB99094.1	EST_HUMAN	b66c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	AB99094.1	EST_HUMAN	b66c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4362	17496	30475	4.28	1.4E-01	AE001710.1	NT	Thermoplasma maritima section 22 of 136 of the complete genome
4531	17689		0.7	1.4E-01	AA776287.1	EST_HUMAN	z60b01.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gbs-X01057_ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4798	17833	30820	0.79	1.4E-01	5453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila); homolog phosphodiesterase E2) (PDE4A), mRNA
5322	18436	31408	0.52	1.4E-01	AJ005180.1	NT	Lycopodium obscurum genomic RAPD band 28
5421	18622	31698	5.21	1.4E-01	T00677.1	EST_HUMAN	ye15c11.s1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31621	4.33	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18644	31622	4.33	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
8427	18666	32881	3.17	1.4E-01	BE32889.1	EST_HUMAN	hm7c02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135538 3'
8811	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
8811	19771	33162	4.46	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6701	19858	33249	3.7	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6715	19873		1.51	1.4E-01	BE266936.1	EST_HUMAN	801193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19886	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
7278	20369		0.71	1.4E-01	AL118568.1	EST_HUMAN	DKFZp701A0910.1 701 (synonym: hamy2) Homo sapiens cDNA clone DKFZp701A0910 5'
7646	20817		1.78	1.4E-01	AW016373.1	EST_HUMAN	UHH-B10-act-c-08-0-UJ.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20888		0.73	1.4E-01	AT762827.1	EST_HUMAN	w04f12.x1 NCL CGAP_CL1 Homo sapiens cDNA clone IMAGE:2389285 3' similar to SW:ICE4_HUMAN P49882 CASPASE-4 PRECURSOR;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20691	34167	0.93	1.4E-01	T63770.1	EST_HUMAN	ye0011.1.2 Stratiogene placenta (#837225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains
7799	20856	34345	0.95	1.4E-01	U85645.1	NT	Alu repetitive element
7832	20982	34490	1.02	1.4E-01	AI305102.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8162	21244		0.54	1.4E-01	BF310288.1	EST_HUMAN	Q90012.1 Soares_NIHMP1_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8670	21750		1.32	1.4E-01	AV689047.1	EST_HUMAN	601894760F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124189 5'
8984	22063		0.8	1.4E-01	AI436093.1	EST_HUMAN	AV689047 GLC Homo sapiens cDNA clone GLCFSH08 3'
9114	22193	35738	4.94	1.4E-01	AA307073.1	EST_HUMAN	tr92812.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
9184	22272	35810	0.76	1.4E-01	AW023636.1	EST_HUMAN	TR-002710 O02710 GAG POLYPROTEIN:
9322	22398	35951	1.07	1.4E-01	R62748.1	EST_HUMAN	EST178182 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22398	35952	1.07	1.4E-01	R62748.1	EST_HUMAN	af58603.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9388	22463	36027	8.62	1.4E-01	BF310959.1	EST_HUMAN	y10105.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:138873 5'
9475	22532	36098	1.72	1.4E-01	W63411.1	EST_HUMAN	y10105.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:138873 5'
9547	22612	36180	0.54	1.4E-01	X73283.1	NT	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9547	22612	36181	0.54	1.4E-01	X73283.1	NT	z64e04.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9558	22623	36194	1.65	1.4E-01	Y10198.1	NT	element KER repetitive element:
9558	22623	36196	1.65	1.4E-01	Y10198.1	NT	M.vannelli genes rpoH, rpoB and rpoA
9649	21082	34607	1.81	1.4E-01	AF121381.1	NT	M.vannelli genes rpoH, rpoB and rpoA
10009	23047	36641	0.54	1.4E-01	X66082.1	NT	Homo sapiens PHEX gene
10192	23229	36821	0.88	1.4E-01	AF023813.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (JAL), and
10293	23328	36831	0.81	1.4E-01	AW021908.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10293	23328	36832	0.91	1.4E-01	AW021908.1	EST_HUMAN	C.porfingens ORF for putative membrane transport protein
10463	23498	37109	0.76	1.4E-01	BF376285.1	EST_HUMAN	Macronitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10463	23498	37110	0.76	1.4E-01	BF376285.1	EST_HUMAN	partial cds
10680	23714		0.91	1.4E-01	T04288.1	EST_HUMAN	af28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485084 5'
10825	23858	37481	0.7	1.4E-01	Z99117.1	NT	af28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485084 5'
10948	24030		1.32	1.4E-01	AA911480.1	EST_HUMAN	MR3-ST0218-211298-013-e08 ST0218 Homo sapiens cDNA
11081	24156	37793	2.57	1.4E-01	R63400.1	EST_HUMAN	MR3-ST0218-211298-013-e08 ST0218 Homo sapiens cDNA
11282	24348	37985	1.68	1.4E-01	AW104882.1	EST_HUMAN	MR3-ST0218-211298-013-e08 ST0218 Homo sapiens cDNA
11354	24416	38071	1.68	1.4E-01	T06102.1	EST_HUMAN	y447003.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:111365 5'
							Bacillus subtilis complete genome (section 14 of 21): from 2632461 to 2812870
							ca89803.s1 NCL_GGAP_GC81 Homo sapiens cDNA clone IMAGE:1320384 3'
							y70c05.r1 Soares breast 2NHF181 Homo sapiens cDNA clone IMAGE:154088 5'
							xl73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							y647g10.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:120630 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11354	24416	38072	1.58	1.4E-01	T88102.1	EST_HUMAN	ye47g10.11 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:120830 5'
11356	24418	38076	2.36	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24627	38306	1.85	1.4E-01	X68092.1	NT	C. parvovirus ORF for putative membrane transport protein
11613	20617		1.57	1.4E-01	AW015373.1	EST_HUMAN	UHFBI0-est-c-09-Q-U1s1 NCI_OGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PHLIP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
12580	25382	32038	4.09	1.4E-01	X74773.1	NT	P.salina plastid gene ecyY
12574	25390		3.28	1.4E-01	11868117	NT	Rattus norvegicus desmin (Des), mRNA
12605	25405		1.71	1.4E-01	BE084835.2	EST_HUMAN	601638490R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3885671 3'
12627	26178		2.83	1.4E-01	BE519302.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834328 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homodog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12742	25483		4.02	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002865
12834	26183		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25812		1.45	1.4E-01	X69192.1	NT	V.plantifolia mRNA for methyltransferase
13084	25977		3.36	1.4E-01	D82863.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25765		1.68	1.4E-01	AW377898.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
332	13546	26578	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13546	26577	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26759	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13839	26866	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUINLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUINLV/Girlington/83/UK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUINLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUINLV/Girlington/83/UK
867	14043	27108	1.55	1.3E-01	X63330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14082	27157	1.26	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1052	14218	27274	2.14	1.3E-01	AL117078.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL116265.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27462	1.67	1.3E-01	AV1712467.1	EST_HUMAN	AV1712467 DCA Homo sapiens cDNA clone DCAAF05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1805	15048	28159	1.02	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Bathyia chinensis strain T4 cDNA library under conditions of nitrogen deprivation
							Rhodospirillum rubrum acidophila pucB5, pucA5, pucB6, pucA6, pucA7, pucA8 and pucC genes and ORF151
2239	15372		1.09	1.3E-01	AJ243578.1	NT	RC4-ST0173-191089-032-412 ST0173 Homo sapiens cDNA
2364	15495		1.38	1.3E-01	AW612104.1	EST_HUMAN	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2455	16583		3.31	1.3E-01	AE001018.1	NT	Carcassius auratus keratin type I mRNA, complete cds
2653	15776	28889	2.78	1.3E-01	M86918.1	NT	Homo sapiens transcription factor KHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3440	16808	28628	1.21	1.3E-01	AF196779.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3816	16976	29679	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3816	16976	29680	0.85	1.3E-01	AP000001.1	NT	Homo sapiens DD4 gene for dihydrolipoyl transacylase 4 [AKR1C4], exon 2
3822	16982	29685	1.55	1.3E-01	AB032169.1	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (F99), mRNA
3905	17064	30063	0.88	1.3E-01	6978940	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4098	17251		1.08	1.3E-01	AL161581.2	NT	Human calicivirus HUJLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJLV/Girlington/83/UK
4162	13839	28866	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUJLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJLV/Girlington/83/UK
4162	13839	28867	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUJLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJLV/Girlington/83/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV9-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA
4281	17426	30416	1.82	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	XV23110.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813896 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21672.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30776	2.54	1.3E-01	BE272339.1	EST_HUMAN	601128098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890083 5'
4748	17883	30865	0.73	1.3E-01	BF078654.1	EST_HUMAN	602154308F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.78	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1165000 nt. position (617)
							ha07606.x1 NC1_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5440	18640	31619	1.01	1.3E-01	AW468888.1	EST_HUMAN	L1 repetitive element
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0083-100400-189-a06 UM0083 Homo sapiens cDNA
5618	18612		0.92	1.3E-01	AF107793.1	NT	Emeticella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	18835		0.87	1.3E-01	AF058880.1	NT	Hepatitis C Virus 68_C1.10 genome polyprotein gene, partial cds
6842	18032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32621	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32622	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4177233 5'
6812	19772	33163	18.92	1.3E-01	AB031326.1	NT	Schistosoma haematobium pomb gene for Alp41, complete cds
6898	18856	33246	2.28	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	2833 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33828	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868079 5'
6974	20202	33829	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868079 5'
7155	20289		0.74	1.3E-01	BF528560.1	EST_HUMAN	602044345F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4181868 5'
7412	20490		1.97	1.3E-01	H48694.1	EST_HUMAN	y33a02.1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:207075 5'
8146	21228		0.70	1.3E-01	BE272339.1	EST_HUMAN	601126095F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8160	21242	34762	1.08	1.3E-01	11423294	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
8192	21274	34797	1.32	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8469	21650	35080	0.86	1.3E-01	11421558	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YD1054c
8580	21661		4.98	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8726	21805	35342	1.26	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	y39g11.1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN;
9420	22494	36060	0.69	1.3E-01	11068003	NT	y39g11.1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9420	22494	36061	0.69	1.3E-01	11068003	NT	SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN;
9672	22834	36204	4.19	1.3E-01	AF023126.1	NT	Plutella xylostella granulovirus, complete genome
9673	23012		0.73	1.3E-01	N89348.1	EST_HUMAN	Plutella xylostella granulovirus, complete genome
10257	23282		1.07	1.3E-01	8363940	NT	Oryctolagus cuniculus H+K4-ATPase alpha 2c subunit mRNA, complete cds
10335	23370	36980	0.95	1.3E-01	AW651688.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
10603	23804	37244	1.08	1.3E-01	AL103246.2	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10743	23778	37389	0.65	1.3E-01	AU121237.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10797	23830	37454	0.45	1.3E-01	AW247838.1	EST_HUMAN	MR2-C10222-201069-001-e01 C10222 Homo sapiens cDNA
10868	23963		2.31	1.3E-01	BF330898.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11455	24515		1.34	1.3E-01	BF092708.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11629	24595		3.2	1.3E-01	6871745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11616	24607	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251948 5'
11616	24607	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251948 5'
11805	24683	38581	7.96	1.3E-01	BE279449.1	EST_HUMAN	601158032F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24985		1.41	1.3E-01	AF912836.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619384.1	EST_HUMAN	601473366F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3978208 5'
12062	25033	38739	1.52	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4300883 5'
12398	25279	32080	2.13	1.3E-01	BE618348.1	EST_HUMAN	601482741F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368		6.39	1.3E-01	AJ242780.1	NT	Gallus gallus acyl1 gene for lysozyme, exons 1-3
12684	25627		1.31	1.3E-01	AB028829.1	NT	Ephydra flumetilis mRNA for sALK-8, complete cds
12995	25647		1.87	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Scores: Dictyostelium discoideum ORF: DG1016 gene, partial cds TR:O60287 O60287 KIAA0639 PROTEIN.;
394	13631	26688	13.87	1.2E-01	A421744.1	EST_HUMAN	tf39602.x1 NCI_CGAP_Brnc23 Homo sapiens cDNA clone IMAGE:2086539 3' similar to gb:U05760_mari
437	13237		1.42	1.2E-01	U68912.1	NT	ANNEXIN V (HUMAN);
501	13753		3.82	1.2E-01	AF039442.1	NT	Dictyostelium discoideum ORF: DG1016 gene, partial cds
1408	14662	27636	2.32	1.2E-01	AU149148.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14582	27637	2.32	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14588		3.35	1.2E-01	AV735249.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1419	14672		0.94	1.2E-01	AL445068.1	NT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1536	14699		0.94	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5 cl48c09.x1 Scores: NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16871
1680	14812	27887	1.1	1.2E-01	Q14834	SWISSPROT	Q16871 ANTIMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.;
1682	14834	27919	2.88	1.2E-01	A1265402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4)
1808	14957		25.75	1.2E-01	X68211.1	NT	q6809.x1 NCI_CGAP_E602 Homo sapiens cDNA clone IMAGE:1900553 3'
1970	15113		1.66	1.2E-01	AW448388.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2253	15386	28514	1.66	1.2E-01	BF249480.1	EST_HUMAN	UIH-B13-est-e-10-0-UI.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734554 3'
2450	15576		0.99	1.2E-01	Z21405.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2656	15779	28893	1.84	1.2E-01	AW988556.1	EST_HUMAN	HSA:AAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA
2905	16063	29098	1.16	1.2E-01	U18018.1	NT	QV3-BN0046-220300-128-F10 BN0046 Homo sapiens cDNA
2987	16143	28162	1.9	1.2E-01	A1720470.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds ss80c09.x1 Barcode colon HPLRB7 Homo sapiens cDNA clone IMAGE:2336024 3' similar to gb:U05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3001	16177	29198	3.44	1.2E-01	M16394.1	NT	Human creatine kinase-B mRNA, complete cds
3068	16244	29266	0.91	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.52	1.2E-01	AW370688.1	EST_HUMAN	QV71-3T0259-26T099-021-405 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U97800.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	16774	29789	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16783		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3895	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810788R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4063668 3'
4298	17441	30428	2.1	1.2E-01	Z94265.1	NT	P. claridii mRNA; repeat region (ID 2MR17)
4298	17441	30427	2.1	1.2E-01	Z94255.1	NT	P. claridii mRNA; repeat region (ID 2MR17)
4431	17571	30552	0.59	1.2E-01	M15891.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. suavis mitochondria ori
5364	18567	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282850 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	
5425	18826	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	2c08d02.r1 Soares_papillary_tumor_NH-HPA Homo sapiens cDNA clone IMAGE:321699 5'
5484	18883	31700	1.65	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31865	1.14	1.2E-01	Z48234.1	NT	M. domestica Barth. Granny Smith adh mRNA for alcohol dehydrogenase
6329	18500	32858	1.9	1.2E-01	BE620945.1	EST_HUMAN	60149351BF1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	18546	32803	0.81	1.2E-01	PT0842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6408	19596	32962	2.28	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6493	19659	33022	1.62	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6561	19723	33101	0.58	1.2E-01	AA747635.1	EST_HUMAN	nc85c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1268024 3'
6785	19940	33338	1.18	1.2E-01	BF347885.1	EST_HUMAN	602023112F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4168388 5'
7154	20288	33731	0.64	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7154	20288	33732	0.64	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
							Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts ddbp76, ddbp76 gamma, ddbp76 alpha and ILF3)
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	
8076	21168		1.13	1.2E-01	BE007072.1	EST_HUMAN	FM3-BN0137-290300-002-00 BN0137 Homo sapiens cDNA
							nc85g03.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
8149	21231	34751	2.45	1.2E-01	AI913753.1	EST_HUMAN	Q88795 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
8197	21278	34801	0.64	1.2E-01	Q02369	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CH-B22)
8504	21585	35119	0.58	1.2E-01	AI832581.1	EST_HUMAN	sa17b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377436 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8590	21671		10.76	1.2E-01	AW083952.1	EST_HUMAN	pc49407.x1 NC1_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:U13452 LAMIN A (HUMAN);
8611	21691		3.78	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	36286	1.09	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8849	21729	36287	1.09	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8887	21986		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8920	21989		0.77	1.2E-01	X15191.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9771	22767	36338	1.3	1.2E-01	X77981.1	NT	S. cerevisiae HXT5 gene
10209	23245	36335	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
11125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24383		3.03	1.2E-01	BE962324.2	EST_HUMAN	6016557851 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38284	2.78	1.2E-01	AF180483.1	NT	Homo sapiens dynein intermediate chain DNAIL1 (DNAIL1) gene, exon 17
11593	24646	38328	1.72	1.2E-01	R40249.1	EST_HUMAN	Y180-c02 s1 Soares Infant brain (NIH) Homo sapiens cDNA clone IMAGE:28880 3'
11798	24788		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV699333.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
12522	25355		4.37	1.2E-01	AJ271736.1	NT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW138) (CD138 ANTIGEN)
12614	26126	31544	2	1.2E-01	Q04912	SWISSPROT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds
12732	25488		1.65	1.2E-01	AF188892.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12734	13753		18.32	1.2E-01	AF039442.1	NT	R. norvegicus NFR88 gene for 68kDa neurofilament
12863	25574		1.4	1.2E-01	X63981.1	NT	gn20g05.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12968	25629	31861	4.89	1.2E-01	A1298903.1	EST_HUMAN	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12992	25644		3.46	1.2E-01	L10187.1	NT	GYCLIN 1
12997	26050		6.44	1.2E-01	O98453	SWISSPROT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13031	25678	31060	1.47	1.2E-01	AE004428.1	NT	Chrysobacterium meningosepticum G0B-1 carboxypeptidase gene, complete cds
13221	25795		1.23	1.2E-01	AF090141.1	NT	hm18d08.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
578	13770	26782	1.96	1.1E-01	A1591003.1	EST_HUMAN	nm08g11.s1 NC1_CGAP_Oo10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_mn1
690	13815	26838	1.33	1.1E-01	AA569003.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1079	14245	27302	1.81	1.1E-01	BF697308.1	EST_HUMAN	602128847F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4288771 5'
1109	14274		1.85	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
1186	16031	27405	3.67	1.1E-01	AW972158.1	EST_HUMAN	EST1384142 MAGE resequencing, MAGL Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2888787-3002865
1549	14701	27780	2.75	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2255	15388		1.73	1.1E-01	AJ069701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2688	15519		2.02	1.1E-01	8758215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2693	15999		1.08	1.1E-01	6878678	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2633	15756		1.27	1.1E-01	AW821808.1	EST_HUMAN	RC0-ST0378-210100-032-g04 ST0379 Homo sapiens cDNA
2917	16095	29107	0.89	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit (Irfca, Genomic, 700 nt, segment 4 of 5)
3098	16274	29288	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1nf02 3'
3422	16591		1.55	1.1E-01	8753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caena1g), mRNA
3508	16876	29685	2.09	1.1E-01	BE303186.1	EST_HUMAN	601308078F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29716	1.47	1.1E-01	X82195.1	NT	C. reinhardtii nuclear gene on linkage group XX
							y62g08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3580	16745	29783	0.71	1.1E-01	R96946.1	EST_HUMAN	Alu repetitive element
3673	16836	29848	0.7	1.1E-01	Y07696.1	NT	A. limnerius gene for transposase
3791	16852		0.96	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	16881	29985	1.28	1.1E-01	X52708.1	NT	G. gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30358	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
4233	17380		0.83	1.1E-01	AF030001.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
4397	17510		11.45	1.1E-01	AF157086.1	NT	Drosophila melanogaster klaricht protein (klar) mRNA, complete cds
4401	17644	30528	0.76	1.1E-01	AW802056.1	EST_HUMAN	U5-UM0070-020500-088-e08 UMA0070 Homo sapiens cDNA
							Type-1 integral membrane protein TAPA-1 (Irfca, B cell lymphoma line 39C13, Genomic, 1973 nt, segment 1 of 7)
4782	17897	30877	0.82	1.1E-01	S44657.1	NT	A. limnerius gene for transposase
4853	18083	31059	1.23	1.1E-01	Y07696.1	NT	A. limnerius gene for transposase
							Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
5134	17380		0.75	1.1E-01	AF030001.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
							nt78a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5787	18879		2.59	1.1E-01	AA747218.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	19047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32383	0.87	1.1E-01	AL110985.1	NT	Bdtryle chiresea strain T4 cDNA library under conditions of nitrogen deprivation
5827	19113	32425	0.98	1.1E-01	BF339518.1	EST_HUMAN	602039170F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5827	19113	32426	0.98	1.1E-01	BF339518.1	EST_HUMAN	602039170F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5838	19144	32459	1.70	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5852	19177	32498	5.15	1.1E-01	M86533.1	NT	Providencia reifertii penicillin G amidase gene
6150	19326	32671	1.88	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32683	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6181	19387	32716	7.73	1.1E-01	AW853698.1	EST_HUMAN	RC3-CT0254-280989-011-e01 CT0254 Homo sapiens cDNA
6554	19716	33082	0.61	1.1E-01	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6582	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19702	33150	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg76d08.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6742	19898	33289	3.88	1.1E-01	O69035	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19906	33684	2.73	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6834	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7193	20058	33498	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	20217	33498	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7456	20845	34007	1.01	1.1E-01	BF382758.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050683 5'
7706	20771	34255	0.98	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt, position (8/7)
7706	20771	34256	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140870F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20688	34391	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140870F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7872	20926	34391	2.16	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7873	20926	34391	0.64	1.1E-01	Z14088.1	NT	B.subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433	3.06	1.1E-01	AA788784.1	EST_HUMAN	af31b06.s1 Soares_parathyroid_tumor_NbHFA Homo sapiens cDNA clone 1240403 3' similar to gic-J03483
8155	21237	34758	1.58	1.1E-01	U67492.1	NT	CHROMOGHRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.66	1.1E-01	AA483574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35013	1.56	1.1E-01	AA483574.1	EST_HUMAN	ih04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:945382
8449	21530	35059	1.26	1.1E-01	X91233.1	NT	ih04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:945382
8489	21570	35059	0.94	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
8546	21627	35165	2.31	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-r08 ST0270 Homo sapiens cDNA
9018	22097	35637	5.67	1.1E-01	U02482.1	NT	DKFZp547P194.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P194 5'
							Pedococcus aceticacid H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element.
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA182153.1	EST_HUMAN	zp93b12.r1 Stratiene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9243	22320	35864	2.26	1.1E-01	AA192163.1	EST_HUMAN	zp93b12.r1 Stratiene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9335	22411	35864	0.71	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and angf gene
9368	22441	36001	2.78	1.1E-01	T72873.1	EST_HUMAN	yd19h03.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.83	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.99	1.1E-01	BE142303.1	EST_HUMAN	CM3-H170142-271069-028-g11 HT0142 Homo sapiens cDNA
9666	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-e08 GN0027 Homo sapiens cDNA
10114	23152		0.77	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10410	23445		1.23	1.1E-01	R80590.1	EST_HUMAN	y86a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3'
10544	23579	37188	1.28	1.1E-01	U60528.1	NT	Ceratitis capitata jojo retrotransposon gag-like, pol-like and env-like genes, complete cds
10914	23987	37631	1.38	1.1E-01	AF245277.1	NT	Dicotyledon discoidium kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	R3265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1n02 3'
11162	24233		2.47	1.1E-01	AF169032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
11300	24388	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	yh3f612.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11483	24542	38212	2.6	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE002074.1	EST_HUMAN	601576924F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3859688 5'
11586	24639	38319	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24966		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25289		3.78	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120800-014-403 NT0112 Homo sapiens cDNA
12849	25910		3.18	1.1E-01	BE974556.1	EST_HUMAN	601680851R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25738	31947	1.98	1.1E-01	BF299753.1	EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.61	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1301	14457	27523	2.18	1.0E-01	AI895498.1	EST_HUMAN	w60401.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2488577 3' similar to contains MERT.53
1423	14577	27650	2.3	1.0E-01	AL161504.2	NT	MERT repetitive element;
2558	15983	28908	1.01	1.0E-01	AW481385.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3813	16973	28678	1.11	1.0E-01	BF239818.1	EST_HUMAN	UH4-B3-alc-4-07-Q-JL.s1 NC1_CGAP_Sub03 Homo sapiens cDNA clone IMAGE:2736420 3'
4054	17220	30228	2.6	1.0E-01	BF365703.1	EST_HUMAN	601806489F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:4134071 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4627	17665	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae APC8, section 91 of 94 of the complete genome
4677	17812		0.78	1.0E-01	A1782349.1	EST_HUMAN	en32cd4.y6 Cassini Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
5030	18187	31143	2.17	1.0E-01	AW652344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5281	18380	31346	0.61	1.0E-01	BE389100.1	EST_HUMAN	601288959F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613532 5'
5436	18636		9.49	1.0E-01	W88490.1	EST_HUMAN	zh62h04.s1 Soares fetal_liver_spleen_TNFRS1_S1 Homo sapiens cDNA clone IMAGE:410895 3'
5534	18731		0.67	1.0E-01	X54015.1	NT	X.campestris genes for sensor and regulator protein
6001	19186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00066 protein, partial cds
6148	19326	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32963	0.9	1.0E-01	AA481879.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:766258 3' similar to contains
6479	19846	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	L1.13.L1 repetitive element;
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7914	20665		2.39	1.0E-01	Y12488.1	NT	yf34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
8118	21200	34721	0.89	1.0E-01	AA881091.1	EST_HUMAN	M.musculus wtn gene
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:3634182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.96	1.0E-01	AW180797.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9387	22482	36028	1.12	1.0E-01	AF102856.2	NT	x09501.x1 NCI_QGAP_UH4 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17208 40S
9695	22744	36314	0.87	1.0E-01	R44963.1	EST_HUMAN	REBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element;
9707	22766		1.9	1.0E-01	M76729.1	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9750	22888		3.15	1.0E-01	AE001501.1	NT	Rattus norvegicus synapto SAPAP-interacting protein Synapton mRNA, complete cds
9764	22761	36331	0.55	1.0E-01	W01955.1	EST_HUMAN	Human pro-alpha-1 (V) collagen mRNA, complete cds
10028	23084	36691	1.88	1.0E-01	BF240154.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10139	23177	36774	8.82	1.0E-01	AB046798.1	NT	z066i10.s1 Soares fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:327282 3'
10347	23382		1.08	1.0E-01	AW957423.1	EST_HUMAN	60150681F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10351	23386	36696	0.62	1.0E-01	T51952.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10537	23572	37179	1.27	1.0E-01	BE782750.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
							y023a06.s1 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
							601594604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839098 5'
							AUT69127 THYR01 Homo sapiens cDNA clone THYR01000895 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37691	2.17	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11288	24352	37692	2.17	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11695	24894	38374	3.64	1.0E-01	BE780543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3896734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Salai-VT1) inserted region, substrain:RIMD 0508952
12364	25633		1.73	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12608	26408		1.73	1.0E-01	7682165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12639	26119		3.11	1.0E-01	U82691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12973	25633		1.8	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	26085		25.82	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25729		6.53	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2838	15983	28060	0.98	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkar-II) mRNA, complete cds
2847	15981	29070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15981	29071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16513	29328	1.31	9.9E-02	AF095910.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
7110	18536	31492	8.06	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
8099	21181	34689	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2599528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
8099	21181		0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2599528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
9457	22573	38139	1.35	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Fltp), mRNA
12132	25112	38816	3.67	9.9E-02	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
577	13769		2.18	9.9E-02	X56338.1	NT	O. sativa RAmg6C gene for alpha-amylase
3214	16388	29398	3.66	9.9E-02	AF184274.1	NT	Deaues cardia leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.9E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.9E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.9E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.16	9.9E-02	M61943.1	NT	Human laminin B1 chain gene, exon 25
11747	23633	37559	1.73	9.9E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3984287 5'
12332	26240		1.29	9.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14538	27611	1.92	9.7E-02	AB005808.1	NT	Alse arborescens mRNA for NADP-malic enzyme, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15499	28601	2.59	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-024 HT0516 Homo sapiens cDNA
4091	17240		4.05	9.7E-02	Q89786	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5481	18981	31639	0.59	9.7E-02	AF089189.1	NT	Caalbacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5481	18981		0.59	9.7E-02	AF089189.1	NT	Caalbacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6138	19316	32957	1.39	9.7E-02	AW054476.1	EST_HUMAN	EST1366548 MAGC resequences, MAGC Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22788.1	EST_HUMAN	yw41c03.s1 Weizmann Offshoot Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22788.1	EST_HUMAN	yw41c03.s1 Weizmann Offshoot Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	A0953984.1	EST_HUMAN	wx78508.x1 NCI CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2649747 3' similar to gb:52851_ma1
11472	24531		1.72	9.7E-02	U56837.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligandin (Lgln) mRNA, partial cds
2073	15213	28330	1.33	9.8E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2073	15213	28331	1.33	9.8E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4484	17604	30982	0.67	9.8E-02	Z32886.2	NT	Proctus mirabilis fibrillar operon, strain H14320
5117	18244	31209	0.95	9.8E-02	AW966230.1	EST_HUMAN	EST1378303 MAGC resequences, MAGC Homo sapiens cDNA
6231	19406		2.76	9.8E-02	BE910039.1	EST_HUMAN	60149808F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900166 5'
8017	21068		0.78	9.8E-02	6878763	NT	Mus musculus lymphocyte antigen 78 (Ly78) mRNA
8571	21652		0.65	9.8E-02	AU137094.1	EST_HUMAN	AU197084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9744	22808	36388	1.49	9.8E-02	AV687898.1	EST_HUMAN	AV687898 OKG Homo sapiens cDNA clone GKCAAH02 5'
10076	23114		1.34	9.8E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916363 5'
10245	23280	36876	1.04	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877	1.04	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.62	9.8E-02	BF677270.1	EST_HUMAN	602085769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10354	23389	36998	1.56	9.8E-02	AB013985.1	NT	Anthrithum majus transposon Tami3 pseudogene for transposase (in S-5 copy)
10354	23389	36999	1.56	9.8E-02	AB013985.1	NT	Anthrithum majus transposon Tami3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.8E-02	P08174	SWISSPROT	COMPLEMENT DEGRADATION ACCELERATING FACTOR PRECURSOR (CD55)
10681	24060	37694	5.27	9.8E-02	Z70702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 1027/82
12019	25003	38704	2.8	9.8E-02	AA625755.1	EST_HUMAN	zid91g01.s1 Soares_beside_NHT Homo sapiens cDNA clone IMAGE:745392 3'
13015	25668		1.7	9.8E-02	H14598.1	EST_HUMAN	ym191003.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48853 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31849	1.41	9.6E-02	AJ288624.1	NT	Gallus gallus ALPHA 10 nAChR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17386	30355	2.16	9.5E-02	AW082395.1	EST_HUMAN	CM2-BN0023-050200-087-412 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7455	20532	34008	4.64	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34282	7.77	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8084	21146	34686	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34687	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.6E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.6E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	25084		1.82	9.5E-02	7657416	NT	Mus musculus odd Ozherm-in homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.85	9.4E-02	BF671063.1	EST_HUMAN	602160882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
3985	17142	30147	4.64	9.4E-02	Z33059.1	NT	M. capricornum DNA for CONTIG MC073
6447	19814	32978	0.95	9.4E-02	AF097963.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7769	20827	34318	0.89	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p35 gene, partial cds
8798	21878		2.5	9.4E-02	Z46883.1	NT	Achoetabacter sp. eyeD, cobQ, sodM, lyeS, rubA, rubB, estB, oxyR, ppk, mtpA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p35 gene, partial cds
12214	26011		7.72	9.4E-02	U31816.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13188	25780	31836	4.84	9.4E-02	U27688.1	NT	Human pepsinogen-1 (Pepsinogen-1) mRNA, complete cds
3054	16230		2.37	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESP1), mRNA
3328	18602	29521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133088F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288289 5'
4288	17413	30400	3.17	9.3E-02	BE381943.1	EST_HUMAN	6012860382F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4288	17413	30401	3.17	9.3E-02	BE381943.1	EST_HUMAN	6012860382F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4657	17890		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5779	18971		0.87	9.3E-02	AP001507.1	NT	Bacillus halodurans genome DNA, section 1/14
8442	21623	35052	0.56	9.3E-02	AW566007.1	EST_HUMAN	EST09 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
8324	22400		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9811	22861	36537	2.3	9.3E-02	BE962831.2	EST_HUMAN	601655688R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3856881 3'
10394	23426	37035	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23426	37036	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10526	23561		3.98	9.3E-02	AW206117.1	EST_HUMAN	UHH-B1-4b-k-05-0-J1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723563 3'
12485	25833		2.08	9.3E-02	AJ248850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
12905	26904		22.03	9.3E-02	AW468850.1	EST_HUMAN	h228h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1 3-galactosyl tr>
13139	28010		2.87	9.3E-02	AF100858.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13480	28486	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13480	28487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13480	28488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54156.1	EST_HUMAN	Y98807.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3247	16421	28437	3.7	9.2E-02	Q28831	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	28564	1.01	9.2E-02	AA634354.1	EST_HUMAN	nt78a01.s1 NCL CGAP_C63 Homo sapiens cDNA clone IMAGE:928136 3'
3676	16839		1.14	9.2E-02	0755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4353	17496		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE289722.1	EST_HUMAN	600844365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:280178 5'
4760	17895	30976	3.44	9.2E-02	X98402.1	NT	G.gallus Mta-CK gene
8188	21280	34802	1.82	9.2E-02	T48920.1	EST_HUMAN	ya89c08.r1 Stragene placenta (#937225) Homo sapiens cDNA clone IMAGE:89808 5' similar to similar to gdx-X96009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X98256.1	NT	H.vulgaris xylose isomerase gene
13120	26201		1.2	9.2E-02	11466872	NT	Podospira ensaeira mitochondrion, complete genome
438	13236	26287	2.23	9.1E-02	X77665.1	NT	O. curvulus K12 keratin gene
3760	16921		0.97	9.1E-02	AW372593.1	EST_HUMAN	PM2-BT0348-161289-001-402 BT0349 Homo sapiens cDNA
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
							Homo sapiens MSH65 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6948	19038	32345	1.23	9.1E-02	AF129756.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7459	26216		0.61	9.1E-02	AF028308.1	NT	sa74a05.y1 Schmeidler fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7549	20619	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	Aeropyrum pernix genomic DNA, section 4/7
7852	20907	34411	0.96	9.1E-02	AF000061.1	NT	Mus musculus thymopodectin zeta mRNA, complete cds
7887	20939	34445	1.02	9.1E-02	U39073.1	NT	Mus musculus gamma adducin gene, exon 9
9124	22203	35746	0.96	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10642	23676		1.46	9.1E-02	T02884.1	EST_HUMAN	FB19F10 Fetal brain, Stragene Homo sapiens cDNA clone FB19F10 3'end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	T6616=Cyl actin [Tripneustes gratilla-sea urchins, embryos, Genbank, 5275 nt]

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-6, and PRL1 genes
11441	24502	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	25121		7.04	9.1E-02	9633404	NT	Bacteriophage MU, complete genome
12393	26124		1.42	9.1E-02	AA179901.1	EST_HUMAN	zp39h12.s1 Strabagene muscle 837209 Homo sapiens cDNA clone IMAGE:611763 3' similar to SW:TRT3_HUMAN P46378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA:
12473	26328		1.32	9.1E-02	AF052665.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12996	26954		13.49	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11
13230	25789		1.27	9.1E-02	AF226888.1	NT	Bombay mori fibrin heavy chain Fib-H (fib-H) gene, complete cds
763	13944	26890	5.99	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1664	14816	27899	7.93	9.0E-02	BE220482.1	EST_HUMAN	h339g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2454	15582	28710	1.18	9.0E-02	AW801364.1	EST_HUMAN	IL5-JM0067-240300-050-H06 UM0087 Homo sapiens cDNA
2864	15978	29088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c086-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15978	29089	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c086-06 from USA envelope glycoprotein (env) gene, partial cds
3417	16588	29803	1.11	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (coe) gene, complete cds
4414	17556	30541	0.6	9.0E-02	S88757.1	NT	corfosteroid-binding globulin [Salimiri sclerous-squirrel monkeys, liver, mRNA, 1474 nt]
4414	17556	30542	0.6	9.0E-02	S88757.1	NT	corfosteroid-binding globulin [Salimiri sclerous-squirrel monkeys, liver, mRNA, 1474 nt]
4790	17925	30913	2.03	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6118	19298	32634	7.2	9.0E-02	W58037.1	EST_HUMAN	z868a12.r1 Soenae_fetal Jung_NbHL10W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR-S52171 S52171 small G protein - human
6860	20012		0.83	9.0E-02	BF082851.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320846 3' similar to contains Alu repetitive element
12819	25546		1.82	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), EscD (escD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Trt (trt), OrfU (orfU), >
1489	14623	27708	1.25	8.9E-02	BF071593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285961 5'
1489	14623	27707	1.25	8.9E-02	BF071593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285961 5'
2460	15587	28714	1.84	8.9E-02	BE153572.1	EST_HUMAN	PMD-HT0339-251189-003-d01 HT0339 Homo sapiens cDNA
4310	17459		1.89	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranF102 protein (AtranF102) gene, partial cds
5972	19158	32474	2.7	8.8E-02	AW452122.1	EST_HUMAN	U1-HB3-alc-f-08-0-U1.e1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32475	2.7	8.8E-02	AW452122.1	EST_HUMAN	U1-HB3-alc-f-08-0-U1.e1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
6987	19172	32484	3.34	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC83107), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20423	33880	1.6	8.0E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE
7731	20763		1.77	8.0E-02	Z76021.1	NT	DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
8240	21322	34839	1.19	8.0E-02	P29475	SWISSPROT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA20F8
8323	21405	34832	0.76	8.0E-02	BF701685.1	EST_HUMAN	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
8323	21405	34833	0.76	8.0E-02	BF701685.1	EST_HUMAN	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8737	21876	35416	5.85	8.0E-02	AA306319.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9819	22859	36439	0.84	8.0E-02	A1289027.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9819	22859	36440	0.84	8.0E-02	A1289027.1	EST_HUMAN	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9934	22873	36503	0.63	8.0E-02	AA339366.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12213	25662		1.8	8.0E-02	P18524	SWISSPROT	MER10 repetitive element;
12366	25262		3.82	8.0E-02	BF695818.1	EST_HUMAN	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
12537	25366		2.75	8.0E-02	6680220	NT	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12584	25393		2	8.0E-02	U28835.1	NT	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12827	26189		1.16	8.0E-02	U40483.1	NT	MER10 repetitive element;
12880	26133		1.54	8.0E-02	AE001514.1	NT	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1404	14558	27632	0.96	8.0E-02	Q27474	SWISSPROT	MYOSIN-2 ISOFORM
4012	17169	30177	1.07	8.0E-02	AA299128.1	EST_HUMAN	602129882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
4145	17297		5.23	8.0E-02	O00288	SWISSPROT	602129882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
4418	17559		0.75	8.0E-02	4680423	NT	Mus musculus hippocampus abundant gene transcript 1 (Hic1), mRNA
7716	20780		0.71	8.0E-02	D17520.1	NT	Human 4-hydroxyphenylpyruvate dioxygenase gene, complete cds
9188	22266	35807	2.07	8.0E-02	AA161872.1	EST_HUMAN	Ceratitis capitata meirner transposon transposase gene, complete cds
11380	24441	38099	2.79	8.0E-02	BE264455.1	EST_HUMAN	Helicobacter pylori, strain J99 section 75 of 132 of the complete genome
11380	24441	38100	2.79	8.0E-02	BE264455.1	EST_HUMAN	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
11541	24597	38273	5.25	8.0E-02	AL040129.1	EST_HUMAN	EST11696 Uterus Homo sapiens cDNA 5' end
12443	25314	32090	1.19	8.0E-02	Z71581.1	NT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) (TAFII130)
3785	16946	29853	4.17	8.7E-02	U82696.2	NT	Homo sapiens paired box gene 6 (enfr16a, keratitis) (PAX6), isoform b, mRNA
							Homo sapiens paired box gene 6 (enfr16a, keratitis) (PAX6), isoform b, mRNA
							Sheep mRNA for angiotensinogen, complete cds
							Sheep mRNA for angiotensinogen, complete cds
							z888a05.s1 Strabagene colon (8637204) Homo sapiens cDNA clone IMAGE:566288 3'
							601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
							601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
							601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
							DKFZp434D1313.1 434 (synonym: htae3) Homo sapiens cDNA clone DKFZp434D1313 5'
							S. cerevisiae chromosome XIV reading frame ORF YNL285w
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xc285TS protein (XO28ORF), and biglycan (BGN) genes, complete cds; and placenta membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16946	29354	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17862	30650	1.4	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000896.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5428	18626	31605	5.49	8.7E-02	AA288875.1	EST_HUMAN	z556g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18628	31608	5.49	8.7E-02	AA288875.1	EST_HUMAN	z556g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6894	20212	33642	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14
6984	20212	33643	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14
7188	20033	33463	0.57	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8046	21128		0.59	8.7E-02	AA284532.1	EST_HUMAN	z220e03.s1 Scores ovary tumor NB-HOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35328	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10851	24033		2.01	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP-4A4) gene, 5' end
11591	24644	38328	1.49	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-Ile and tRNA-Ala genes
12431	25308		2.2	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12848	25432		2.85	8.7E-02	6979057	NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X85292.1	NT	G.gallus mRNA for vigin
1281	14437	27508	7.73	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2317	15448	28591	2.2	8.6E-02	BE408867.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3257	16431	28448	2.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3734	16895		3.69	8.6E-02	AF153362.1	NT	Dicystotellum discoideum adenyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U28187.1	NT	Mus musculus long incubation piron protein (Pmnp) and prion-like protein (Prnd) genes, complete cds
4809	17748	30725	0.66	8.6E-02	U88179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	AB011183.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
6219	18394	32743	4.74	8.6E-02	Y10828.1	NT	Homo sapiens LCN1b gene
6504	19670	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19670	33038	1.26	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34306	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED CBP ACTIVATOR PROTEIN (SRCAP) mRNA
8115	21197	34718	1.09	8.6E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34860	0.56	8.6E-02	11427428	NT	Homo sapiens hypophyseal protein FLJ11006 (FLJ11006), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21406		0.76	8.6E-02	U60186.1	NT	Dicystosellum discoideum proteasome subunit C2 homolog Pric (pric) gene, complete cds
9038	22977	36558	1.24	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jegged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.6E-02	AW662153.1	EST_HUMAN	H20-08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10356	23391	37001	1.07	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37882	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37883	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11627	24583	38259	3.02	8.6E-02	BF305606.1	EST_HUMAN	6071893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.6E-02	BF305606.1	EST_HUMAN	6071893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37834	7.67	8.6E-02	AED01073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11875	24863	38559	2.29	8.6E-02	AF283880.1	NT	Bacillus stearothermophilus BarFI methylase (FIM) and BarFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.58	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.68	8.5E-02	N76915.1	EST_HUMAN	y46808.t1 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:245823 5'
5786	18978	32283	0.73	8.5E-02	AA085491.1	EST_HUMAN	cd83b07.s1 NCI_CGAP_Ku8 Homo sapiens cDNA clone IMAGE:1882917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA C-CHAIN PRECURSOR (HUMAN);
5826	18016		1.59	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 8 PRECURSOR
6135	18314	32653	6.61	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8905	21884	35424	1.98	8.5E-02	6764779	NT	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36980	3.27	8.5E-02	BE633054.1	EST_HUMAN	RCL-OT0037-200700-014-005 OT0037 Homo sapiens cDNA
10041	23079	36981	3.27	8.5E-02	BE633054.1	EST_HUMAN	RCL-OT0037-200700-014-005 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X76731.1	NT	V armodyles gene for armodylokin C
10702	23735	37340	0.82	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.5E-02	AF156510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.5E-02	AB001582.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12873	25888		2.76	8.5E-02	AJ005596.1	NT	Adrenomedullin mRNA for MYB-related transcription factor
13070	25700		2.44	8.5E-02	AA302894.1	EST_HUMAN	EST12736 Ovary II Homo sapiens cDNA 5' end
2732	16070	28981	4.05	8.4E-02	W69330.1	EST_HUMAN	cd44e11.t1 Scores fetal heart NBH19W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18027	31603	9.84	8.4E-02	BE287163.1	EST_HUMAN	601180436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6828	18881	33388	1.46	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8218	21300	34821	6.95	8.4E-02	BE09074.1	EST_HUMAN	GMB-BT0790-280400-162-d05 BT0790 Homo sapiens cDNA
9043	22122	35864	1.16	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	A735184.1	EST_HUMAN	ss8g10.x1 Barsheed colon HFLR87 Homo sapiens cDNA clone IMAGE:2335942 3' similar to TR:O88312
10631	23665		0.48	8.4E-02	A730882.1	EST_HUMAN	O88312 GDB-4.;
12361	26264	32114	1.87	8.4E-02	R79408.1	EST_HUMAN	A730882 HTF Homo sapiens cDNA clone HTFBMG04 5'
3082	16846	28853	7.77	8.3E-02	P76334	SWISSPROT	X63112.1 Soares placenta Nb21-P Homo sapiens cDNA clone IMAGE:145885 5'
3708	16870	29873	0.75	8.3E-02	A436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29874	0.75	8.3E-02	A436797.1	EST_HUMAN	th82g08.x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.88	8.3E-02	M54984.1	NT	th82g08.x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6388	19588	32917	0.74	8.3E-02	A842838.1	EST_HUMAN	C. truncal A2b region open reading frame, complete cds
6488	19682	33025	2.87	8.3E-02	A952883.1	NT	w07911.1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8169	21261	34771	3.08	8.3E-02	AF106787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8202	21264		1.06	8.3E-02	AA895285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8496	21576		1.31	8.3E-02	AA887873.1	EST_HUMAN	cg88g08.s1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.1 L1 L1
9738	22803	36377	1.09	8.3E-02	AW583503.1	EST_HUMAN	repetitive element;
9751	22889		2.02	8.3E-02	AL161698.2	NT	cg91110.s1 NCI CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1682779 3'
10548	23584		0.72	8.3E-02	AF020409.1	NT	la09110.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
12448	28128		1.81	8.3E-02	BE939458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;
1410	14584		9.13	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1525	14878	27759	2.03	8.2E-02	AF167077.2	NT	Dictyostellium discoideum DocA (docA) mRNA, complete cds
3141	16317		1.97	8.2E-02	AL163206.2	NT	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3828683 5'
3904	17063		1.35	8.2E-02	AL161498.2	NT	Gallus gallus mRNA for OBGAM protein gamma isoform
4114	17288	30288	0.89	8.2E-02	AL163208.2	NT	Caris familiaris glutamate transporter (EAAT4) mRNA, complete cds
4389	17542	30523	6.58	8.2E-02	P48880	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4398	17542	30524	6.58	8.2E-02	P48880	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4889	17542	30525	6.58	8.2E-02	P48880	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
5182	18314	31282	9.43	8.2E-02	U76008.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5450	18850	31629	1.49	8.2E-02	BE997030.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7165	20288	33741	3.16	8.2E-02	AF308555.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7810	20882		0.59	8.2E-02	AV743341.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
8905	21984		0.59	8.2E-02	U28397.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
8971	22050	35593	3.24	8.2E-02	AW875128.1	EST_HUMAN	601438678F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824523 5'
9789	22838	36416	4.89	8.2E-02	X04197.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
							AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
							Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
							RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
							Beet necrotic yellow vein virus RNA-2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8985	23004	36899	2.27	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12454	25318	32094	3.83	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AFR39, section 73 of 84 of the complete genome
12686	25498	32021	1.43	8.2E-02	AW862185.1	EST_HUMAN	QV4-CT0361-021209-040-b01 CT0361 Homo sapiens cDNA
12689	25875		2.58	8.2E-02	AF275388.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.86	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6508	19874	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1494F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
7766	20815		0.99	8.1E-02	AI692681.1	EST_HUMAN	wd8098.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8535	21616	35151	0.58	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21616	35152	0.56	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10116	23154		1.83	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
10885	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	xy45b11.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10888	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UIH-B13-eko-g-01-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UIH-B13-eko-g-01-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
g	16003	26246	7.61	8.0E-02	AW964663.1	EST_HUMAN	EST386723 MAGE resequences, MAGE Homo sapiens cDNA
959	14132	27191	0.65	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1733	16046	27974	11.83	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1733	16046	27975	11.83	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1852	15095	28196	4.4	8.0E-02	BE067219.1	EST_HUMAN	PM8-BT0347-170200-001-008 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 17127, 2137258-2267258
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 17127, 2137259-2267259
2541	15668		3.21	8.0E-02	BF246744.1	EST_HUMAN	601655448F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076619 5'
2881	14280	27338	1.55	8.0E-02	M23449.1	NT	Dicystosium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2965	16141	29159	1.05	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 515
3919	17078	30075	0.93	8.0E-02	AW866118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4835	18065		6.87	8.0E-02	X72794.1	NT	Mus musculus gene for galactase B
5038	18168	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, complete cds, and small nuclear RNAs (lRNAs)
6012	19188	32513	3.56	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19186	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34926	2.41	8.0E-02	AL114983.1	NT	Bdtrf1s chinea strain T4 cDNA library under conditions of nitrogen deprivation
8389	22644	36213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
8589	22844	36214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10361	23366		0.49	8.0E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.64	8.0E-02	AF21796.1	NT	Homo sapiens SCG10 like-protein, helixase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.69	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12496	25337	32061	3.54	8.0E-02	AJ006376.1	NT	Drosophila oronia hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	15376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	800943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3043	16219	28240	12.63	7.9E-02	AJ582029.1	EST_HUMAN	ar90608.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4932	18062		1.16	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
6836	18989		1.14	7.9E-02	BF368018.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	RC9-GIN0042-310300-024-d11 GN0042 Homo sapiens cDNA
10234	23269	36859	5.6	7.9E-02	AJ081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of Mif2 Smf4p (SMT4) gene, complete cds
10234	23269	36860	5.6	7.9E-02	AJ081644.1	EST_HUMAN	cu63005.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632466 3' similar to WP:C37A2.2
13008	25664		1.27	7.9E-02	AJ761639.1	EST_HUMAN	CE08811;
1237	14396	27457	1.49	7.8E-02	AJ763276.1	EST_HUMAN	cu63005.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632466 3' similar to WP:C37A2.2
1237	14396	27458	1.49	7.8E-02	AJ763276.1	EST_HUMAN	CE08611;
4915	18045	31035	0.6	7.8E-02	BE636331.1	EST_HUMAN	wg68h01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
5198	17003		2.97	7.8E-02	BE250048.1	EST_HUMAN	cc58d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1670467 5' similar to contains L1:18 L1
							repetitive element;
							cc58d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1670467 5' similar to contains L1:18 L1
							repetitive element;
							PM3-FN0058-140700-005-009 FN0058 Homo sapiens cDNA
							800943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2659693 5'
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7223	20087	33504	1.1	7.8E-02	U82695.2	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exam. SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20067	33505	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and blycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8085	22064	35004	0.83	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3825449 5'
9081	22180	35702	0.69	7.8E-02	X78344.1	NT	S.cerevisiae CAT18 gene
9253	22330	35877	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9361	22703	36269	0.9	7.8E-02	AA468364.1	EST_HUMAN	nc88b06.t1 NCL_GCAP_P1 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36637	0.56	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3998281 to 4214814
10501	23085	37616	2.19	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12910	25002	31979	1.35	7.8E-02	U72847.1	NT	Homo sapiens envelopin (EVPL) gene, exons 15 through 18
1431	16038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16940		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34690	5.98	7.7E-02	AA402949.1	EST_HUMAN	z153d11.r1 Scores every tumor NHOt Homo sapiens cDNA clone IMAGE:741717 5' similar to TR-G1173905 G1173905 SPLICOSOME ASSOCIATED PROTEIN. ;
10040	23078	36679	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36861	0.94	7.7E-02	A1318682.1	EST_HUMAN	ta80b08.x1 NCL_GCAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10336	23371	36862	0.84	7.7E-02	A1318692.1	EST_HUMAN	ta80b08.x1 NCL_GCAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24931	37672	3.98	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3474	16841	26690	3.1	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3494	16861	26673	0.98	7.6E-02	AA269447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' and similar to similar to proboscoidin 43
3648	18812	29825	0.96	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf18 gene and C11orf17 gene
6222	19397	32746	0.89	7.6E-02	A1061275.1	EST_HUMAN	an25g02.x1 Geaster Wilms tumor Homo sapiens cDNA clone IMAGE:1689730 3'
6486	19683	33015	1.14	7.6E-02	BE376328.1	EST_HUMAN	601238402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
8570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10101	23139		0.99	7.6E-02	AL136079.2	NT	Campylobacter jejuni NCTC11108 complete genomes, segment 5/8
10424	23459	37064	0.5	7.6E-02	BE706002.1	EST_HUMAN	RC1-HT0645-020800-017-008 HT0545 Homo sapiens cDNA
10557	23592		1.04	7.6E-02	BE69638.2	EST_HUMAN	601664916F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639810 3'
10815	23848	37469	0.97	7.6E-02	X92656.1	NT	Laccarium mRNA for those phosphate translocator

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	0.97	7.6E-02	X92656.1	NT	Lescularium mRNA for triose phosphate translocator
11874	24959	38861	1.93	7.6E-02	AW986646.1	EST_HUMAN	QV3-BN0046-160400-161-e04 BN0046 Homo sapiens cDNA
807	13987	27039	1.86	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13987	27040	1.86	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1971	15114	28214	0.89	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17768	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5974	19158	32477	1.45	7.5E-02	AI948714.1	EST_HUMAN	wq24f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472267 3'
8533	21614	35150	1.28	7.6E-02	AI884387.1	EST_HUMAN	wf52b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA
8705	21785	35318	1.36	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
10238	28273		0.49	7.6E-02	BF221730.1	EST_HUMAN	AU116813 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10711	23744	37950	0.73	7.5E-02	BF206809.1	EST_HUMAN	7c61c05.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10816	23849	37471	0.82	7.6E-02	X78480.1	NT	MER27 repetitive element;
490	13884	26718	1.41	7.4E-02	AW838647.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1488	14642		1.21	7.4E-02	AF030027.1	NT	Cifini DSM 207113 16S rDNA
2848	15771		0.96	7.4E-02	6759069	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3683	16848	28854	1.21	7.4E-02	AI807885.1	EST_HUMAN	Equine herpesvirus 4 strain NS80567, complete genome
4828	17959	30948	1.19	7.4E-02	L78810.1	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4814	18044	31034	2.65	7.4E-02	L78810.1	NT	w493h01.x1 Soares_NFI_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
5056	18184	31159	4.42	7.4E-02	6878442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
6824	19784		1.89	7.4E-02	R17477.1	EST_HUMAN	Rattus norvegicus Actin receptor like kinase 1 (Acvrl1), mRNA
6717	19875	33288	0.86	7.4E-02	AF030422.1	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
7638	20705	34184	0.84	7.4E-02	AA005132.1	EST_HUMAN	y914g08.f1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
8085	21167	34883	1.11	7.4E-02	BE880112.1	EST_HUMAN	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
8698	21778	35312	1.26	7.4E-02	U56089.1	NT	no71d02.g1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112269 3'
9387	22442	36002	1.08	7.4E-02	AW629805.1	EST_HUMAN	801483398F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885264 5'
9387	22442	36003	1.08	7.4E-02	AW629805.1	EST_HUMAN	Human periodic tryptophan protein 2 (PWPF2) gene, exons 15 to 21, and complete cds
9639	21082	34593	0.58	7.4E-02	AI672839.1	EST_HUMAN	h67d1.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9639	21082	34594	0.58	7.4E-02	AI672839.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
							h67d1.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
							w674d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
							w674d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10019	23067	36663	1	7.4E-02	U62283.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10148	23184	36780	0.49	7.4E-02	BF512678.1	EST_HUMAN	UHF-BW1-ano-g-06-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
11266	24335	37875	1.46	7.4E-02	AA059167.1	EST_HUMAN	z64e01.1 Soares retina N264-R Homo sapiens cDNA clone IMAGE:381720 5'
11014	24001	36604	1.42	7.4E-02	AI125063.1	EST_HUMAN	aa01407.s1 Barstead aorta HPL_R83 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:IM88492
12408	26288		1.22	7.4E-02	11525893	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12692	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12870	26580	31995	2.61	7.4E-02	BF035088.1	EST_HUMAN	GM4-HT0243-081199-037-411 HT0243 Homo sapiens cDNA
12882	25585	31988	1.44	7.4E-02	AJ223469.2	NT	001453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3867738 5'
481	13676	26708	1.15	7.3E-02	BE964961.2	EST_HUMAN	Aspergillus nidulans pmD, pmX, pmA genes
481	13676	26709	1.15	7.3E-02	BE964961.2	EST_HUMAN	001658738R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3868209 3'
702	13885	26917	2.66	7.3E-02	AE001789.1	EST_HUMAN	001658738R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3868209 3'
1510	16040	27748	3.26	7.3E-02	AW900281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1883	16050		15.79	7.3E-02	AL163302.2	NT	CM10-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
5112	18240		1.02	7.3E-02	U12283.1	NT	Homo sapiens chromosome 21 segment HS21C102
6682	19744	33126	1.46	7.3E-02	AA778977.1	EST_HUMAN	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
7633	20702	34180	2.37	7.3E-02	P06143	SWISSPROT	gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7633	20702	34181	2.37	7.3E-02	P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7881	21030		0.58	7.3E-02	BF316067.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8361	21442		1.36	7.3E-02	7682107	NT	001688047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126515 5'
8598	21677	35214	0.5	7.3E-02	Y10887.2	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8411	22485		1.17	7.3E-02	AB011090.1	NT	Mus musculus cdh5 gene, exon 1, partial
11482	19744	33126	1.78	7.3E-02	AA778977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
122	13362	26382	0.5	7.2E-02	AED00882.1	NT	z24e02.s1 Soares fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
122	13362	26383	0.5	7.2E-02	AED00882.1	NT	gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1505	14658	27739	2.5	7.2E-02	AL163301.2	NT	Methanobacterium thermosulfohalophilum from basins 1028155 to 1039834 (section 88 of 148) of the complete genome
1505	14658	27740	2.5	7.2E-02	AL163301.2	NT	Methanobacterium thermosulfohalophilum from basins 1028155 to 1039834 (section 88 of 148) of the complete genome
2614	16738		3.34	7.2E-02	U14794.1	NT	Homo sapiens chromosome 21 segment HS21C101
3891	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
							Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
							UHF-BW0-gje-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4465	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18604	31578	2.78	7.2E-02	U67331.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.76	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217506.1	EST_HUMAN	601883390F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086224 5'
7318	20400	33963	1.32	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7335	20416	33878	0.7	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	6634887	NT	Strongyloides purpuratus mitochondrion, complete genome
8382	21463	34987	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8264	22341		0.57	7.2E-02	Y17217.1	NT	Lactococcus lactis cepE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAU0301 5'
9891	23000	36596	4.88	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23166	36754	0.96	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4029496 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q82340 Q82340
10395	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
							662407.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23595	37201	2.15	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bgllycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10692	23725	37331	5.57	7.2E-02	BE565003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		3.47	7.2E-02	BE530214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10837	23870	37492	0.55	7.2E-02	AA706997.1	EST_HUMAN	z28h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451041 3'
11153	24224	37853	4.14	7.2E-02	AF049874.1	NT	Rattus norvegicus BHLH transcription factor Miel1 (Miel1) gene, complete cds
12316	25230	32104	2.12	7.2E-02	AA773698.1	EST_HUMAN	af81a04.r1 Soares_NihMIPu_S1 Homo sapiens cDNA clone IMAGE:1046398 5'
12350	25253		3.63	7.2E-02	AJ230706.1	EST_HUMAN	AJ230706 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12411	25290		2.05	7.2E-02	AA584465.1	EST_HUMAN	nc05f08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
12474	25327		4.23	7.2E-02	U82628.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12488	25697		7.37	7.2E-02	AW000862.1	EST_HUMAN	GM4-NIN1009-200300-110-c11 NN1008 Homo sapiens cDNA
13048	25687		1.63	7.2E-02	AA401779.1	EST_HUMAN	z57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5'
1953	15096	28187	2.05	7.1E-02	L02280.1	NT	Human Immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2368	15497	28623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4092081 5'
8091	21173	34687	1.06	7.1E-02	AI125284.1	EST_HUMAN	q52a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738922 3'
10896	23898	37521	0.63	7.1E-02	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
12193	25150		6.46	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
641	13734	26758	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1529	14682		1.28	7.0E-02	X06877.1	NT	Martellia Micut-1 gene
1801	14950	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	z166f04.s1 Sitratogene colon (#637204) Homo sapiens cDNA clone IMAGE:5065599 3'
3095	16271	26286	2.02	7.0E-02	AW138152.1	EST_HUMAN	UIH-B11-acy-o-07-0-JUL.e1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718020 3'
4004	17161	30167	0.65	7.0E-02	AA815438.1	EST_HUMAN	a65e12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376678 3' similar to gb:K03002 60S
4155	17307	30301	1.19	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4268	17403		1.14	7.0E-02	AW792862.1	EST_HUMAN	QV4-BT0407-280100-080-e10 BT0407 Homo sapiens cDNA
4330	17473	30458	1.16	7.0E-02	AF077821.1	NT	GM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris Inducible nitric oxide synthase mRNA, complete cds
5493	18692		0.82	7.0E-02	Y09143.2	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7560	20632	34107	0.9	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7782	20838	34331	0.68	7.0E-02	Y19187.1	NT	AV689285 GK Homo sapiens cDNA clone GKCAE06 5'
9299	22375	35928	1.24	7.0E-02	9828113	NT	Gallus gallus mRNA for partial ezrin, XL spliced variant (acz gene)
9797	22837	38416	1.31	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10158	23195	36791	0.88	7.0E-02	U27268.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11654	24733	38424	2.6	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
13022	25673	31958	1.2	7.0E-02	11421638	NT	ah69a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
527	13720	26744	7.08	6.9E-02	AL163210.2	NT	TKHT JUNCTION PROTEIN ZO-1 (HUMAN);
627	13720	26745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20118 (FLJ20116), mRNA
1364	14518		1.58	6.9E-02	4507868	NT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30052	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
5302	18419	31389	4.11	6.9E-02	Z70763.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M04956.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
7793	20649		0.87	6.9E-02	AF164967.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SCpA24F7
8242	21324		1.14	6.9E-02	U12022.1	NT	M.hyalinis 115 kDa protein (P115) gene, complete cds
8750	21829	36396	1.01	6.9E-02	BE567435.1	EST_HUMAN	Canine distemper virus strain A78/17, complete genome
							Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							801340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685050 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8760	21829	35397	1.01	6.8E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9320	22368	35949	0.87	6.0E-02	U22987.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	S81752.1	NT	DIPH2L -candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.46	6.9E-02	S81752.1	NT	DIPH2L -candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25251		10.94	6.9E-02	X74315.1	NT	X laevis XFD2 mRNA for fork head protein
12624	25357		1.58	6.8E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOF2 HOMOLOG
12770	25513		3.37	6.9E-02	AF195863.1	NT	Homo sapiens membrane-bound aminopeptidase P (ANPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA498759.1	EST_HUMAN	es30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gbl:M22382
1932	15075	28178	1.18	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1936	15099	28199	3.85	6.8E-02	AF156873.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4876	17810		0.94	6.8E-02	BE141076.1	EST_HUMAN	WRO-HT0069-071089-001-c05 HT0069 Homo sapiens cDNA
6768	19914		0.85	6.8E-02	P20792	SWISSPROT	CELL SURFACE RECEPTOR DAF-1 PRECURSOR
7040	20093	33981	0.99	6.8E-02	BE061890.1	EST_HUMAN	CELL SURFACE RECEPTOR DAF-1 PRECURSOR
7432	20509	34420	8.22	6.8E-02	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C0068
7891	20915	34420	0.9	6.8E-02	U16858.1	NT	Dicystostellium discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8483	21584	35099	0.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 516
8483	21584	35100	0.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 516
12141	28166		1.47	6.8E-02	T03214.1	EST_HUMAN	FBAA8 Fetal brain, Strategene Homo sapiens cDNA clone FBAA8 3'end similar to LINE-1
12276	25208		1.84	6.8E-02	AA758014.1	EST_HUMAN	ah67705.s1 Soares, testis, NHT Homo sapiens cDNA clone 1320705 3'
12906	25598		1.34	6.8E-02	AW875839.1	EST_HUMAN	EST987948 IMAGE resequences, MAGN Homo sapiens cDNA
12972	25692		2.3	6.8E-02		NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
13203	26091	31660	1.24	6.8E-02	6978885	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1668	14711		2.71	6.7E-02	AF116839.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1*01 allele, complete cds
1942	16086	28186	2.17	6.7E-02	AJ20285.1	EST_HUMAN	9978504.x1 Soares, NFL T, GBC S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3811	16971	29973	4.48	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD-4 (HOXA)
4065	17221	30229	0.74	6.7E-02	U63783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4065	17221	30230	0.74	6.7E-02	U63783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
7969	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	zid20g11.s1 Soares, fetal heart_NhrH19W Homo sapiens cDNA clone IMAGE:341252 3' similar to contains
8034	21117	34635	0.74	6.7E-02	X62895.1	NT	Alu repetitive element; contains element L1 repetitive element;
							H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34638	0.74	6.7E-02	X62895.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35260	0.73	6.7E-02	AW082688.1	EST_HUMAN	pc61c11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2880788 3'
9800	22840	36417	0.58	6.7E-02	AW137359.1	EST_HUMAN	UIH-B11-ecr-g-01-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2716433 3'
9800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UIH-B11-ecr-g-01-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2716433 3'
1378	14534	27608	0.98	6.6E-02	A1735509.1	EST_HUMAN	at12a09.x1 Bartshead acrt HPLR88 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
2282	15385	28513	3.73	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3552	16717	29731	12.38	6.6E-02	R84306.1	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139578 3'
3557	16732	29748	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3567	16732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5083	18221	31191	12.07	6.6E-02	Q81703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31192	12.07	6.6E-02	Q81703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	274407.J1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U4270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6130	18255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	274407.J1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U4270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33284	3.92	6.6E-02	X08411.1	NT	P. vulgaris mRNA for chalcone synthase
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6837	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6837	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8133	21215	34736	1.51	6.6E-02	AF082572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8669	21749	35287	0.77	6.6E-02	AF006055.1	NT	Dicystosellum discoideum clarin (clar) gene, complete cds
8979	22058		0.53	6.6E-02	O60873	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23194	36790	0.54	6.6E-02	AA58752.1	EST_HUMAN	997g06.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
10282	23327	36830	1.51	6.6E-02	Y07948.1	NT	Homo sapiens EWS, gar22, np22 and bcr22 genes
10327	23362		0.65	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.49	6.6E-02	BF604659.1	EST_HUMAN	602080808F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
11205	24274	37811	4.86	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0084-010600-008-472 SN0084 Homo sapiens cDNA
12761	25505		4.64	6.6E-02	9937691	NT	Mus musculus DIPB gene (Dipb), mRNA
13124	25733		1.26	6.6E-02	AF167490.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
606	13785	26805	1.57	6.5E-02	BF027638.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7706088	NT	Homo sapiens E2F-like protein (LOC61270), mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14822	28016	2.04	6.5E-02	AE000784.1	NT	Aquifer acidicus section 98 of 109 of the complete genome
5878	18870	32150	2.07	6.5E-02	AA443991.1	EST_HUMAN	244812.s1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6873	19832	33271	0.73	6.5E-02	BF663340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7113	18539	31493	1.02	6.5E-02	U22681.1	NT	602118887F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278029 5'
10147	23185	36781	0.57	6.5E-02	BE963200.2	EST_HUMAN	Asciobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10147	23185	36782	0.57	6.5E-02	BE963200.2	EST_HUMAN	601666817R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3865687 3'
10883	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3865687 3'
10875	23900	37589	4.45	6.5E-02	AA185648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12163	25120		3.78	6.5E-02	M21496.1	NT	z32g06.s1 Soares NIH-MP Pu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12633	26363		3.67	6.5E-02	AF102963.1	NT	Rabbit microsomal epoxide hydrolase
589	13780	26789	1.48	6.4E-02	X04549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
1770	14918	28013	0.99	6.4E-02	AE001777.1	NT	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermoboga maritima section 88 of 138 of the complete genome
							Thermoboga maritima section 89 of 138 of the complete genome
5568	18783	31803	1.11	6.4E-02	A191958.1	EST_HUMAN	qe07601.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6239	19413	32761	2.64	6.4E-02	AF052733.1	NT	LTR8 repetitive element;
6239	19413	32762	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6532	19686	33088	1.23	6.4E-02	A1672898.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	w973g12.x1 Soares_Dieckgrasse_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
8631	21812		2.47	6.4E-02	6753323	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850503 3'
8866	21944	36478	4.17	6.4E-02	AA093305.1	EST_HUMAN	Mus musculus cheperonin subunit 6a (zeta) (Cct6a), mRNA
8927	22403	35955	0.98	6.4E-02	AF150196.1	EST_HUMAN	K1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9786	22836		0.81	6.4E-02	BE834083.1	EST_HUMAN	AF150196 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9918	22858	36545	1.87	6.4E-02	AB011126.1	NT	RC1-OT0883-150800-014-g06 OT0883 Homo sapiens cDNA
10468	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10468	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24993	38697	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRat gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12008	24933	39938	1.88	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mitch 5B (MUC5B) gene, partial cds
12479	25331	32056	2.61	6.4E-02	AJ27174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF106905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc20h gene, partial cds; smRNP, G7A, NC23, MUS homolog, CLOP, NQ24, NG25, and NG26 genes, complete cds; and unknown genes
3992	19854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6284	19439	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873318F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.84	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9481	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
10218	23254	36843	3.52	6.3E-02	AB070182.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKG Homo sapiens cDNA clone GKGAHE01 5'
10854	19438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873318F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15674	28797	1.04	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4365	17508	30489	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17940		5.68	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (ROSS-A) (RO52)
6935	20250	33695	0.78	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7805	20681	34354	0.88	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8018	21087		0.68	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	28226		0.92	6.2E-02	M81101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22809	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_t01a19_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9881	22730	36300	1.19	6.2E-02	6677898	NT	Mus musculus striatal cell derived factor receptor 2 (Sdr2), mRNA
11415	24476	38140	1.42	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Melanizum antisense mRNA for Chymotrypsin (chyl) gene
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12617	25415		1.24	6.2E-02	BE703085.1	EST_HUMAN	601983773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3637842 5'
12703	25467	32024	3.61	6.2E-02	BF112639.1	EST_HUMAN	737008.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523816 3' similar to
268	13485	26616	3.63	6.1E-02	D16471.1	NT	TR-00VLS6 Q9V4S8 HYPOTHETICAL 30.3 KD PROTEIN. [1]:
4099	17284		2.85	6.1E-02	U73325.1	NT	Human mRNA, Xq terminal portion
							Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8468	21539	35068	3.65	6.1E-02	X00268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21840	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8861	21840	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10867	24048	37681	3.9	6.1E-02	BE176543.1	EST_HUMAN	IL3-H10816-110500-138-C08 HT0618 Homo sapiens cDNA
12134	25114	38818	1.86	6.1E-02	AB025333.1	NT	Epitratrus burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26053		30.03	6.1E-02	X70988.1	NT	S. japonicum mRNA for serine-enzyme
12836	25957		1.58	6.1E-02	A188691.1	EST_HUMAN	tz56707.X1 NCI_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2282801 3'
12863	25945		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1291	14447	27513	1.58	6.0E-02	AE001777.1	NT	Thermoplasma maritima section 89 of 136 of the complete genome
2740	15857	28689	1.17	6.0E-02	AW088848.1	EST_HUMAN	EST380824 IMAGE resequences, MAGJ Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocricetus auratus mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.t1 Stratagene HeLa cell c3 637216 Homo sapiens cDNA clone IMAGE:626310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.t1 Stratagene HeLa cell c3 637216 Homo sapiens cDNA clone IMAGE:626310 5'
3301	16476	29498	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3301	16476	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE864443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-B10253-011189-013-504 BT0253 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	A1807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element;
7127	18553	31467	2.86	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7127	18553	31468	2.86	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7338	20418	33880	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4049226 5'
7857	20912	34417	1.78	6.0E-02	A1204275.1	EST_HUMAN	qf58h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754189 3'
8617	21687		0.46	6.0E-02	11468495	NT	Reclinomonas americana mitochondrion, complete genome
9472	22529	36092	1.29	6.0E-02	A1623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.29	6.0E-02	A1623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9806	22681	36233	2	6.0E-02	AJ245365.1	NT	Actpenser basii partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9806	22681	36234	2	6.0E-02	AJ245365.1	NT	Actpenser basii partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309767.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' and similar to similar to heat shock protein 1, 60 kDa-like

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA308797.1	EST_HUMAN	EST180854: Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.t1 Stragapene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X089181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
12921	25606		5.12	6.0E-02	A1809273.1	EST_HUMAN	wf89h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60289
239	13481	28489	5.88	5.9E-02	AW834719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN:
3048	16224	29246	2.77	5.9E-02	AF190289.1	NT	RC1-DT0001-230100-012-e10 DT0001 Homo sapiens cDNA
4864	17897		0.77	5.9E-02	AF16811.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
8817	21898	35435	2	5.9E-02		NT	Duck parvovirus strain 80-2183 capsid protein (VP3) gene, partial cds
9650	21093		0.97	5.9E-02	8055249	EST_HUMAN	Mus musculus iraqi related homeobox 5 (Drosophila) (hox), mRNA
11026	24104		7.39	5.9E-02	BF242748.1	EST_HUMAN	601877608F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4105994 5'
11855	24824		1.35	5.9E-02	6079870	NT	Mus musculus foliata-like (Fol), mRNA
11850	24839		1.57	5.9E-02	BF572539.1	EST_HUMAN	6020765-48F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
1693	14845	27929	0.97	5.8E-02	D90110.1	NT	Gallus gallus HKC9 telomere junction
3763	16914	29817	1.68	5.8E-02	O61768	SWISSPROT	Thiobacillus ferrooxidans mcrC, mcrA genes and URF-1
4474	17614	30593	6.79	5.8E-02	AE001776.1	EST_HUMAN	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	Thermotoga maritima section 87 of 138 of the complete genome
4669	17804	30792	4.64	5.8E-02	A1247505.1	EST_HUMAN	w24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4698	17804	30763	4.64	5.8E-02	A1247505.1	EST_HUMAN	w24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4698	17831		2.1	5.8E-02	AF098284.1	NT	qh5601.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1846897 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
7855	20910	34414	2.76	5.8E-02	M68180.1	NT	(Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7855	20910	34415	2.76	5.8E-02	M68180.1	NT	Human polymorphic microsatellite DNA
8868	21945	35479	0.61	5.8E-02	AL163283.2	NT	Human polymorphic microsatellite DNA
12965	26261		1.65	5.8E-02	AF220177.1	NT	Homo sapiens chromosome 21 segment HS21C083
12681	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
3123	16289	29312	1.14	5.7E-02	A1081844.1	EST_HUMAN	nc76e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3139	16316	29328	1.09	5.7E-02	AF119117.1	NT	cu63105.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1032465 3' similar to WP:C37A2.2
3902	17061	30060	2.3	5.7E-02	AW686791.1	EST_HUMAN	CE086111
4807	17941		0.95	5.7E-02	M95099.1	NT	Homo sapiens dopamine transporter (SLC3A3) gene, complete cds
						EST_HUMAN	EST378868 IMAGE resequences, MAGI Homo sapiens cDNA
						NT	Bos taurus lysozyme gene (cow 3), complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.87	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20699	34175	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851885 5'
7630	20699	34176	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851885 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10056	23083	36695	0.82	5.7E-02	6681280	NT	Mus musculus act2 oncogene (Ect2), mRNA
11464	24523	38193	3.14	5.7E-02	A1752885.1	EST_HUMAN	cm18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm18b09 random
11464	24523	38194	3.14	5.7E-02	A1752885.1	EST_HUMAN	cm18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm18b09 random
12588	25988		1.86	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12769	25512		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12853	26042		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
13012	26165		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13171	25769	31929	5.21	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein E gene, complete cds
1556	14709	27789	1.18	5.7E-02	R48513.1	EST_HUMAN	X164d10.s1 Soares breast 2NtHBst Homo sapiens cDNA clone IMAGE:163523 3' similar to contains L1 repetitive element;
2362	15493		1.1	5.6E-02	AF094455.1	NT	Hydroxycylo retundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4783	17898	30878	1.95	5.6E-02	BE904308.1	EST_HUMAN	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896610 5'
4818	17951	30938		5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6789	19854	33354	1.37	5.6E-02	AA280599.1	EST_HUMAN	zs46c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
7031	20187	33589	1.31	5.6E-02	AA280599.1	EST_HUMAN	x02c10.x1 NCI_CGAP_UK2 Homo sapiens cDNA clone IMAGE:2696050 3' similar to TR:O84878 O94879 KIAA0905 PROTEIN;
7301	20383	33642	5.87	5.6E-02	AW172708.1	EST_HUMAN	cd47712.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
8010	21060	34572	1.02	5.6E-02	AA868182.1	EST_HUMAN	QVO-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8002	22081	35623	3.3	5.6E-02	BE008001.1	EST_HUMAN	q664g11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1704308 3'
9002	22081	35624	1.32	5.6E-02	A1183583.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
10017	23055	36651	2.52	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
			2.52	5.6E-02	BE542663.1	EST_HUMAN	nt48d07.s1 NCI_CGAP_AVI Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768859 G768859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11863	24851		2.42	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	15838	28948	7.33	6.6E-02	X97889.1	NT	H. sapiens gene encoding La autoantigen
3286	10460	29481	3.33	5.9E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.9E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5776	18968	32272	3.49	5.9E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18968	32272	4.32	6.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.9E-02	6755902	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8311	21393	34917	0.87	5.9E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21393	34918	0.87	5.9E-02	AF170911.1	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36478	0.78	5.9E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36477	0.78	5.9E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9851	22890	36583	1.24	6.6E-02	U68492.1	NT	Mus musculus second L11 receptor alpha chain (L11Ra2) gene, exons 1 and 2
11271	24339	37977	6.31	5.9E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
3084	18280		0.85	5.4E-02	AJ277468.1	NT	Oryza sativa ribb3-1 gene for putative Bowman Birk trypsin inhibitor
3509	18478		8.19	5.4E-02	BE073468.1	EST_HUMAN	RCS-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4020	17177	30186	0.61	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8316	21398		1.18	5.4E-02	Z89118.1	NT	Bacillus subtilis complete genome (section 13 of 21); from Z395261 to Z813730
9271	22347	35807	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37853	1.86	5.4E-02	U20790.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-160700-021-D08 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-160700-021-D06 FN0112 Homo sapiens cDNA
12463	26880		3.72	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.56	5.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA
1535	14688	27768	20.67	6.3E-02	T64769.1	EST_HUMAN	ye3712.1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01503
2566	15991	28810	3.22	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Pseudomonas putida tpsS gene
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster lambrin B2 gene, complete cds
3221	16395	29406	4.83	6.3E-02	AJ276408.1	NT	Drosophila melanogaster lambrin B2 gene, complete cds
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31612	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5434	18634	31613	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6228	19403	32763	1.14	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20180	33580	4.02	5.3E-02	9885413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33769	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7517	20690		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8081	21073	34585	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHEICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
8600	21681		0.68	5.3E-02	U10098.1	NT	Mus musculus 128/Sv cystatin C (cst8) gene, complete cds
8325	22401	35954	1.73	6.3E-02	X03127.1	NT	Podospora anserina mitochondrial psalman-sea DNA
10482	23497		0.61	5.3E-02	Y07807.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postembryogenesis, 20-28 hpf)
10538	23573	37180	0.70	6.3E-02	X68432.1	NT	B. rerio pou3f mRNA for transcription factor
13173	25761	31831	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	15488		64.04	5.2E-02	5031908	NT	Homo sapiens mcpin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	16358	28363	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	28364	2.39	6.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17206	30216	0.8	5.2E-02	AF238101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crt1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nkr-1 mRNA, complete cds
5287	18406	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32545	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.94	5.2E-02	AB090965.1	EST_HUMAN	wj80e04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to cortical MER15.b71
							MER15 repetitive element;
							DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
7424	20601	33872	1.23	5.2E-02	P36322	SWISSPROT	Homo sapiens chromosome 21 segment HS21C004
8388	21470		2.39	5.2E-02	AL163204.2	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
8631	22971	36580	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
8631	22971	36561	2.16	6.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25463		1.6	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2437	15565		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp47D0073_1 647 (synonym: h181) Homo sapiens cDNA clone DKFZp47D0073 5'
5161	18283	31248	0.89	5.1E-02	BE587423.2	EST_HUMAN	601653555R2 NIH MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6251	18372		0.96	5.1E-02	AL138077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
5349	18462		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	18986	33370	0.78	5.1E-02	AF280368.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6897	19519	31608	1.73	5.1E-02	BF37825.1	EST_HUMAN	QVD-UM0051-250800-350-608 UM0051 Homo sapiens cDNA
8447	21523	35055	0.82	6.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21523	35055	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131866.1	NT	Spodoptera littoralis mRNA for 3-dehydroxyisone 3beta-reductase
8086	22165	35710	0.63	6.1E-02	P02633	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	6.1E-02	P02633	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36846	4.27	5.1E-02	AF012888.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37028	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487	20721	1.81	5.1E-02	AF082467.1	NT	Quercus imelo polygalacturonase precursor (MPC3) mRNA, complete cds
495	13690	20721	2.8	5.0E-02	AF082467.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	16188	28299	5.08	5.0E-02	P02810	SWISSPROT	4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2879	14182	27244	10.68	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucosyltransferase (UGT2B13) mRNA, complete cds
3418	16567		1.38	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3684	16947		1.01	5.0E-02	U82782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3775	16936	28942	5.9	5.0E-02	U12769.2	NT	Arthraea permy period clock protein homolog mRNA, complete cds
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6258	19432	32779	0.84	5.0E-02	AF086284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
8438	19605		1.28	5.0E-02	AJ242825.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7128	18554	31469	0.93	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7708	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7913	20864		0.87	5.0E-02	AW082484.1	EST_HUMAN	MRO-CT0084-100899-002-g10 CT0084 Homo sapiens cDNA
10403	23438	37045	1.37	5.0E-02	AF305238.1	NT	Mus musculus Fos-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10956	23988		0.95	5.0E-02	BF213280.1	EST_HUMAN	601844753F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4070101 5'
11782	24772	36468	2.26	6.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
12220	26004		4.7	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
231	19452		11.82	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	19588	26623	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
380	13588	20624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2837	16114	29128	0.71	4.9E-02	U32036.1	NT	Zea mays phytyl synthase (Y1) gene, complete cds
3360	16532	29548	1.85	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3680	16823		0.85	4.9E-02	AA188940.1	EST_HUMAN	z48a12.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832928 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
3681	16844	26851	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	16844	26852	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4684	18063	31068	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg66g10.x1 NCI CGAP UM4 Homo sapiens cDNA clone IMAGE:2632386 3'
4684	18063	31070	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg66g10.x1 NCI CGAP UM4 Homo sapiens cDNA clone IMAGE:2632386 3'
6488	18885	31702	1.92	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
6488	18885	31703	1.92	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7282	20374	33831	1.79	4.9E-02	AE000680.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21894		1.07	4.9E-02	AE002308.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8842	22021		0.81	4.9E-02	BE831532.1	EST_HUMAN	MIR0-HT0408-170800-003-a08 HT0408 Homo sapiens cDNA
8954	22033	36576	0.97	4.9E-02	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.84	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37459	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24686	38378	3.46	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	25624		3.23	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26582	1.19	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26582	2.81	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13686	26726	11.83	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	26810	2.08	4.8E-02	W51983.1	EST_HUMAN	z48a02.s1 Soares, senescent, fibroblasts_NHFSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:U30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3280	16454	28476	1.79	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4788	17928		1.08	4.8E-02	Z84280.1	NT	S.scrofa gene for skeletal muscle myosin receptor
5237	18359	31328	0.98	4.8E-02	U61914.1	NT	Streptococcus constellatus D-alanine D-alanine ligase gene, partial cds
8332	21414	34940	1.41	4.8E-02	AW388487.1	EST_HUMAN	MIR2-S10128-221088-012-b02 S10128 Homo sapiens cDNA
8329	22405	35657	1.01	4.8E-02	AJ001388.1	NT	Fugu rubripes rps24 gene
8329	22405	35658	1.01	4.8E-02	AJ001388.1	NT	Fugu rubripes rps24 gene
11219	24288	37828	1.84	4.8E-02	X61238.1	NT	S.cerevisiae NUM1 gene, involved in nuclear migration control
11219	24288	37829	1.84	4.8E-02	X61238.1	NT	S.cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.8E-02	9832863	NT	Streptococcus thermophilus bacteriophage Sif19, complete genome
5122	18248	31214	0.74	4.7E-02	6881261	NT	Rattus norvegicus Nedd9 (Nes), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6969	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	y29709.1 Soares melanocyte 2NtHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
7025	20161	33581	0.89	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.89	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8445	21628	35053	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB028678.1	NT	Gallus gallus Wpct-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9636	22875		0.7	4.7E-02	A1873042.1	EST_HUMAN	we7ec10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLC8KD02 3'
281	13488	26531	0.89	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13939	26884	2.89	4.6E-02	AED00445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476		1.49	4.6E-02	A014255.1	EST_HUMAN	em5002.e1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR.P00533
1390	14644	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	P00533 LIMA ; contains element LTR1 repetitive element ;
2557	15652	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
2869	13488	26531	1.78	4.6E-02	BE153583.1	EST_HUMAN	xr2403.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2684653 3' similar to SW:GRF1_HUMAN
3073	16249	29270	0.84	4.6E-02	BE153583.1	EST_HUMAN	O12849 G-RICH SEQUENCE FACTOR-1 ;
3416	16249	29270	0.89	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3555	16249	29270	0.94	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17395		0.92	4.6E-02	AF220385.1	NT	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5852	19042	32348	1.67	4.6E-02	AF076982.1	NT	Mus musculus nuclear RNA helicase II/Gu (dxb21) gene, complete cds
6359	19529	32887	3.67	4.6E-02	X61624.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	G. rehnhardti ep2 (ep8) mRNA
6359	19529					NT	G. rehnhardti ep2 (ep8) mRNA
6936	20251	33687	1.41	4.6E-02	AH49574.1	EST_HUMAN	gc00000.x1 Soares_placenta_8t9weeks_2NtHP6b9W Homo sapiens cDNA clone IMAGE:1713071 3'
8007	21057	34568	0.83	4.6E-02	6978720	NT	similar to contains L1.13 L1 repetitive element ;
8856	21835	35472	3.81	4.6E-02	BE154006.1	EST_HUMAN	Rattus norvegicus Cathespain H (Cath), mRNA
11689	24687	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
						EST_HUMAN	cl27109.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13078	25708		3.14	4.6E-02	X57808.1	NT	Human germ-line immunoglobulin lambda light chain gene
480	13665	26693	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1245	14404	27468	1.62	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1847	14993	28095	4.93	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3817	16977	29881	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6360	18530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6636	19795	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7018	20154	33575	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8587	21688	35207	2.24	4.5E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10155	23192	38788	4.2	4.5E-02	A325216.1	EST_HUMAN	EST28167 Carcinosarcoma II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10305	23340	38946	0.47	4.5E-02	X95508.1	NT	A. europaeum mRNA for legumin-like protein
10421	23456	37081	0.79	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 Integrin, complete cds
12442	25313	32089	2.61	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFP13), mRNA
12891	26051	31684	3.79	4.6E-02	AA191097.1	EST_HUMAN	z045f11.1 Strabagene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:632493 5'
227	13449	27273	4.35	4.4E-02	BE072783.1	EST_HUMAN	601652154F1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:2936386 5'
1050	14216		0.77	4.4E-02	L18295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2163	15289		6.82	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2559	15894	28809	1.81	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3730	16891	28895	1.69	4.4E-02	AF159160.1	NT	Mycobacterium xenopus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30866	1.33	4.4E-02	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7267	20350	33802	0.59	4.4E-02	AF095824.1	NT	Caris familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7267	20350	33803	0.59	4.4E-02	AF095824.1	NT	Caris familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA798669.1	EST_HUMAN	nc13n03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11328	24389	38034	2.64	4.4E-02	AF080689.1	NT	Hepatitis E virus strain HEV-US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	aa33104.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897831 5'
12158	25126		4.55	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
12347	26182		1.65	4.4E-02	BF241245.1	EST_HUMAN	601878748F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
802	13982	27034	7.25	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	26671	1.55	4.3E-02	AF704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3516	16682	29683	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6829	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6825	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA662288.1	EST_HUMAN	ns58c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188898
8711	21791	35327	0.69	4.3E-02	AF283369.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35821	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	22080	35822	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.2	4.3E-02	AL139077.2	NT	Campylobacter jejuni NCTC11109 complete genome, segment 4/6
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	14065		2.4	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
919	14094	27159	1.51	4.2E-02	AW003646.1	EST_HUMAN	w234q01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1768	14907		1.37	4.2E-02	AL445068.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.53 L1 L1 repetitive element ;
1819	14988	28060	0.89	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome, segment 4/5
3754	18915	28918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4895	17898	30862	0.59	4.2E-02	BF342985.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
							602017105F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4152872 5'
5735	18828	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 49 (CYP3A49) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18828	32225	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 49 (CYP3A49) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31480	0.61	4.2E-02	BE268285.1	EST_HUMAN	Homo sapiens cytochrome P450 polypeptide 49 (CYP3A49) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7896	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34267	0.61	4.2E-02	AF730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAV104 5'
9010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-66)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	24361	38002	1.52	4.2E-02	AA978118.1	EST_HUMAN	cr33b11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1650481 3' similar to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24840	38320	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11587	24840	38321	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11785	24785	38483	1.52	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV38 envelope glycoprotein gene, complete cds
12728	28109		6.64	4.2E-02	AF188349.1	EST_HUMAN	w49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
13076	25705		1.17	4.2E-02	D14711.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
523	13716	28743	1.85	4.1E-02	AF200628.1	NT	Homo sapiens HPS1 gene, intron 5
2741	15858	28970	1.06	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30168	0.61	4.1E-02	BE297238.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4005	17162	30169	0.61	4.1E-02	BE297238.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4595	17732		8.4	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-184-103 NN0012 Homo sapiens cDNA
5229	18351		0.91	4.1E-02	X85880.1	NT	L monocytogenes type 3 partial lap gene (strain 443)
5759	18951	32263	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5759	18951	32264	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7022	20158		0.98	4.1E-02	X75881.1	NT	A. freilana mRNA for plasma membrane intrinsic protein 1a
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7682	20747	34228	1.79	4.1E-02	7682347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20992	34502	2.81	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8402	21483	35011	0.74	4.1E-02	P97887	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8845	21924	35482	0.79	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
8855	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13112	28110	31688	9.81	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plesid glutamine synthetase, exons 1-12
3316	16488	29507	3.85	4.0E-02	AB040804.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3800	17050	30058	1.09	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5495	18894	31710	5.31	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52107.x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:368380 3' similar to TR:O75286.O75288 R29124.1.;
7887	20921	34428	5.99	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homodog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7829	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20963	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20963	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7960	21029	34543	0.61	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9844	22884		0.63	4.0E-02	BF076378.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
9869	22908	36495	2.46	4.0E-02	AJ001094.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thid:umarate reductase subunit A
10190	23227		1.08	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for CcpA ATPase
12353	26908	31859	18.34	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1144	14309	27368	2.79	3.9E-02	BF16149.1	EST_HUMAN	U1H-BW1-emb-h-08-0-LJ1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1376	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2016	15158	28281	3.22	3.9E-02	AJ403366.1	NT	Mimulus DNA for cleavage-binding fragment DesD7
2769	18884		1.97	3.9E-02	4506882	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-17189-021-Q09 S10258 Homo sapiens cDNA
5270	18398	31368	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5279	18398	31367	0.8	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5849	18039	32346	1	3.9E-02	BE088841.1	EST_HUMAN	601849874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933842 5'
5977	18162	32482	0.65	3.9E-02	BF076203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049630 5'
8023	21106	34623	1.44	3.9E-02	BF236613.1	EST_HUMAN	601606848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8250	21332	34849	0.6	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8250	21332	34850	0.6	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11695	21071	34582	1.58	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	26059		3.54	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12938	25506		2.35	3.8E-02	U80091.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1T, TCRBV11S1A1T, HVB refc, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
13036	25979		64.89	3.8E-02	AL049898.2	NT	Mus musculus chromosome X contigB1; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmx28orf
5556	18754	31782	0.8	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6212	19397	32798	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
7471	20546	34018	1.72	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8864	21943		1.51	3.8E-02	M80675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10789	23822	37446	0.64	3.8E-02	7682563	NT	Homo sapiens PRO0614 protein (PRO0514), mRNA
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1016	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2310	15442	28577	6.19	3.7E-02	A084806.1	EST_HUMAN	wf85e08.x1 NC1_CGAP_KID11 Homo sapiens cDNA clone IMAGE:2494502 3'
2645	16768	28883	0.97	3.7E-02	A018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3115	16291	29308	1.13	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3117	16293	29307	4.33	3.7E-02	BF312863.1	EST_HUMAN	601896233F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4125584 5'
3543	16708		0.91	3.7E-02	6880544	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
7726	28216		0.95	3.7E-02	AP000068.1	NT	Aeropyrum pernix genomic DNA, section 9/7
7869	20023	34430	0.81	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10219	23256		1.01	3.7E-02	AA782516.1	EST_HUMAN	ai55c08.s1 Soares parathyroid tumor_NbH1PA Homo sapiens cDNA clone 1360912 3'
12227	25176	38837	7.41	3.7E-02	BF124874.1	EST_HUMAN	601782117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12861	25945	31764	3.71	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
13058	25688		1.23	3.7E-02	11467432	NT	Odonatalia alenata chloroplast, complete genome
3744	16905	29809	0.82	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3752	16913	29816	0.9	3.6E-02	AL068806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q28.3) of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL068810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q28.3) of Homo sapiens
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldhyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldhyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase

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5617	18811	31880	0.68	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
6846	19898	33408	4.48	3.6E-02	AW946518.1	EST_HUMAN	GM2-EN0013-110500-182-b10 EN0013 Homo sapiens cDNA
6846	19899	33407	4.48	3.6E-02	AW945510.1	EST_HUMAN	GM2-EN0013-110500-182-b10 EN0013 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cy2 precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	hw20a05.s1 NCL CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2
7811	20868	34360	0.94	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8591	22846	36216	2.18	3.6E-02	U20608.1	NT	MR0-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
8591	22846	36217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
8591	22846	36217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.84	3.6E-02	BF947688.1	EST_HUMAN	602020453F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158118 5'
11456	24516	36183	1.48	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11456	24516	36184	1.48	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14093	27158	0.99	3.5E-02	U09506.1	NT	Drosophila melanogaster figgrin mRNA, complete cds
1033	14202	27260	2.43	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPTX1) gene, complete cds
1595	14748	27831	1.4	3.5E-02	BF678085.1	EST_HUMAN	6020885136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1595	14748	27832	1.4	3.5E-02	BF678085.1	EST_HUMAN	6020885136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.5E-02	AE001773.1	NT	Thermoboga maritima section 85 of 138 of the complete genome
4435	17676	30556	1.11	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6351	19521	32878	1.76	3.5E-02	J01238.1	NT	Mizus actin 1 gene (MACT), complete cds
8165	21247		0.91	3.5E-02	H25951.1	EST_HUMAN	jp44a05.r1 Soares retina N2b54HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element
8824	21903	35443	2.53	3.5E-02	BE989970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3828737 3'
10224	23280	36948	0.94	3.5E-02	X76942.1	NT	L.lactis MG1363 grpE and dnaK genes
10270	23305	36902	0.51	3.5E-02	BE581042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775	38471	1.78	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291288-002-H03 CT0328 Homo sapiens cDNA
11785	24775	38472	1.78	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291288-002-H03 CT0328 Homo sapiens cDNA
12878	25583		1.31	3.5E-02	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S8P to TORBV21S2A2 region
12955	25901		2.71	3.5E-02	BE276848.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
592	13783	26802	47.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
592	13783	26803	47.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
693	13783	28803	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FL100113 protein, partial cds
1078	14242	27288	2.57	3.4E-02	AW274020.1	EST_HUMAN	3028d07.x1 Soares_NFL_T_03C_S1 Homo sapiens cDNA clone IMAGE:2814283 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR:
1233	14332		5.43	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2485	15522		1.7	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER28 repetitive element
3617	16683	28694	1.5	3.4E-02	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4030	17186	30186	3.72	3.4E-02	AW784952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59799.1	NT	Musculus S-antigen gene promoter region
5172	18284		1.9	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5180	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6983	18512	31604	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8458	21537		3.15	3.4E-02	A1889629.1	EST_HUMAN	w182d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35587	1.18	3.4E-02	AA084886.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element/contains element MER25 MER26 repetitive element;
							zq04f11.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9118	22187		5.28	3.4E-02	AA194306.1	EST_HUMAN	IPSGKPLPKVTLSDRGVPLKATMRNFTEITAENLTINLKESVTADAGRYEITAAANSSGTTKAFINIVLDRPG
9880	23019		0.66	3.4E-02	A1092718.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGSQVNTYLLKRETSATVWTEVSATVARTMMKVKML ...;
383	13591		6.8	3.3E-02	AA396735.1	EST_HUMAN	cc0h08.x1 Soares_parathyroid tumor_NhHPA Homo sapiens cDNA clone IMAGE:168519 3'
1183	14365	27413	12.43	3.3E-02	AB035987.1	NT	z76c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1688	14821	27804	1.23	3.3E-02	AF110783.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1778	14927		1.37	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LM-protein 1 (FHIL1) gene, complete cds
2149	15285		2.02	3.3E-02	R09112.1	EST_HUMAN	Aquifex anaerobius section 32 of 109 of the complete genome
3445	16813	29631	0.86	3.3E-02	H02395.1	EST_HUMAN	yf28c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4283	14821	27804	3.74	3.3E-02	AF110783.1	NT	y85h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4589	17726	30709	2.24	3.3E-02	BF245905.1	EST_HUMAN	Homo sapiens skeletal muscle LM-protein 1 (FHIL1) gene, complete cds
6580	19722	33089	25.73	3.3E-02	BF245905.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Trp1), mRNA
6580	19722	33100	25.73	3.3E-02	BF245905.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7677	20742	34223	0.83	3.3E-02	AF124162.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8523	22586	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (mcs) gene, partial cds
8523	22588	36158	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m82d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9024	22879	36248	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Scores_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9624	22879	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Scores_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11383	24444	38104	3.28	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:121101 5'
12428	25303		3.1	3.3E-02	T96545.1	EST_HUMAN	ye49f11.1 Scores fetal liver spleen TNF18 Homo sapiens cDNA clone IMAGE:4332497 5'
12567	25379		1.6	3.3E-02	AF289885.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12591	25398		1.85	3.3E-02	M81890.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
134	13360	26394	1.79	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1160	14314	27370	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68a allele, complete cds
1150	14314	27371	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68b allele, complete cds
1812	14981	28054	1.08	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2802	13360	26394	0.87	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3204	16379	29389	13.21	3.2E-02	BE867353.1	EST_HUMAN	60142431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4334	17477		16.42	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4890	18020	31005	3.85	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
6310	18427	31397	0.93	3.2E-02	AW850159.1	EST_HUMAN	IL3-CT0219-271099-022-004 CT0219 Homo sapiens cDNA
5652	18846	32127	1.49	3.2E-02	X68709.1	NT	S.grissoecarneau wHG-Stv gene
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	S.grissoecarneau wHG-Stv gene
6653	18812	33200	2.4	3.2E-02	M32437.1	NT	Ratipolymavirus left junction in cell line W98.14
6656	19815		30.91	3.2E-02	T89387.1	EST_HUMAN	yc33h12.s1 Scores fetal liver spleen TNF18 Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element;
6743	19899	33290	3.7	3.2E-02	AF173845.1	NT	Sagurus oedipus tissue kallikrein gene, complete cds
7639	20989	34499	0.82	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8496	21577	35113	8.04	3.2E-02	6890568	NT	Mus musculus kinesin family member 3c (KIF3c), mRNA
9141	22220		0.67	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9426	22500	36065	1.2	3.2E-02	AZ78971.1	EST_HUMAN	qm17604.x1 NCI CGAP_L15 Homo sapiens cDNA clone IMAGE:1882063 3'
9426	22500	36066	1.2	3.2E-02	AZ78971.1	EST_HUMAN	qm17604.x1 NCI CGAP_L15 Homo sapiens cDNA clone IMAGE:1882063 3'
10262	23297		4.51	3.2E-02	AAT19795.1	EST_HUMAN	zq54b12.s1 Scores_pituitary_gland_NHHPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb1.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10566	23901	37207	1.11	3.2E-02	U96782.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14446		1.92	3.1E-02	4503418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27569	1.48	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	6871664	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18380	31449	1.28	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5478	18376		2.6	3.1E-02	AA278478.1	EST_HUMAN	z881a08.f1 NCI_CGAP_G0281 Homo sapiens cDNA clone IMAGE:703858 5'
5764	18566	32259	0.77	3.1E-02	BF68742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066789 5'
8122	21204		0.68	3.1E-02	AV69098.1	EST_HUMAN	AV69098 GKC Homo sapiens cDNA clone GKCAVH09 5'
8142	22221	35764	0.48	3.1E-02	BE66082.2	EST_HUMAN	601658578F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886281 3'
8339	22415	35968	0.48	3.1E-02	AB72302.1	EST_HUMAN	wn57d09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36884	2.67	3.1E-02	AF034778.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1852	14805		2.41	3.0E-02	AF187125.1	NT	Plyoktines mitrulus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2852	15775	28889	1.08	3.0E-02	AA02242.1	EST_HUMAN	z65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
3743	16904	28808	2.82	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16998		0.93	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0288-150200-040-909 ST0288 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA384003.1	EST_HUMAN	EST74530 Pituitary gland II Homo sapiens cDNA 5' end
5164	18286	31260	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5164	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.57	3.0E-02	N98615.1	EST_HUMAN	z838a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element ;
6384	19553	32911	0.57	3.0E-02	N98615.1	EST_HUMAN	z838a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element ;
6829	20244	33677	2.87	3.0E-02	AJ242806.1	NT	Gyprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)
7047	20100	33516	2.9	3.0E-02	BE689948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE689948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20456	33921	1.22	3.0E-02	M86524.1	NT	Human dystrophin gene
8317	21369		0.48	3.0E-02	BF079706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286684 5'
8821	21800	35439	0.55	3.0E-02	BE512670.1	EST_HUMAN	601171628F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545047 5'
8842	21821	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HTT0704-290800-108-c04 HTT0704 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8893	22072		1.93	3.0E-02	AF275554.1	NT	Omlthorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37319	2.03	3.0E-02	AE001787.1	NT	Thermobia maritima section 109 of 138 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24556	38243	2.28	3.0E-02	M81367.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11889	24874	38678	7.11	3.0E-02	AA483218.1	EST_HUMAN	ne878D.s1 NC1 CGAP K181 Homo sapiens cDNA clone IMAGE:3911263
12538	26168	31556	1.95	3.0E-02	R32018.1	EST_HUMAN	y163004.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12943	25821		11.82	3.0E-02	AW885565.1	EST_HUMAN	QV4-NIN0038-270400-187-h08 NN0038 Homo sapiens cDNA
12989	26161		4.97	3.0E-02	AF049887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3050	16813	28826	0.9	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30206	0.81	2.8E-02	H72805.1	EST_HUMAN	y007610.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6421	19590	32855	8.58	2.9E-02	BF032233.1	EST_HUMAN	601432081F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5'
7398	20478	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7584	20558	34133	0.65	2.8E-02	D28214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8187	21269	34783	0.82	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis glucanate-6-phosphate dehydrogenase (gnd) gene, partial cds
8187	21268	34784	0.82	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis glucanate-6-phosphate dehydrogenase (gnd) gene, partial cds
8659	22899	35482	2.14	2.9E-02	AW876979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
8859	22899	35483	2.14	2.9E-02	AW876979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW976597.1	EST_HUMAN	EST1388706 MAGE resequences, MAGN Homo sapiens cDNA
10553	23588	37106	1.25	2.9E-02	AP000084.1	NT	Aeropyrum pernix genomic DNA, section 777
11303	16813	29826	1.44	2.9E-02	X66294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU195817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002982 5'
579	13771		0.78	2.8E-02	AW970183.1	EST_HUMAN	EST1382234 MAGE resequences, MAGK Homo sapiens cDNA
3453	16620	29639	1.2	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3453	16620	29640	1.2	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
4430	17570		0.78	2.8E-02	8393761	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5905	18890	31886	11	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
6948	20261	33689	1.08	2.8E-02	T78680.1	EST_HUMAN	y021008.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108855 5'
8523	21604	35142	1.67	2.8E-02	AJ005820.1	NT	Ornithostigma plantaginum mRNA for homeodomain leucine zipper protein (hb-1)
8219	22297	35940	0.76	2.8E-02	AA280762.1	EST_HUMAN	zs96c08.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711486 5'
9409	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	36144	0.76	2.8E-02	AE001082.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9574	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9574	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
							Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13SS, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S913S2>
1518	14671	27753	0.96	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3518	16684	29695	1.99	2.7E-02	AL161494.2	NT	Y96H12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30447	1.93	2.7E-02	NA47258.1	EST_HUMAN	Y96H12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	NA47258.1	EST_HUMAN	Y96H12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5382	18555	31432	0.6	2.7E-02	BF245672.1	EST_HUMAN	601864811F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5557	18755	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	Y93309.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SF-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6022	18205	32525	0.69	2.7E-02	X61670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
6734	19690		1.02	2.7E-02	X97660.1	NT	A.bisporus pgIA gene
7213	20078	33491	1.92	2.7E-02	AA93571.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624681 3'
8549	21630		1.36	2.7E-02	AB77036.1	EST_HUMAN	contains Alu repetitive element;
8516	21805	35434	0.55	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
885	13776	26796	2.62	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1399	14553		0.99	2.6E-02	AW650516.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2439	15567	26694	2.6	2.6E-02	AA460021.1	EST_HUMAN	ab02b02.2.1 Stratagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:839585 3'
2441	15569	26696	4.45	2.6E-02		NT	Mus musculus histidine rich calcium binding protein (Hir), mRNA
2441	15569	26697	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hir), mRNA
					6754241	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, C6, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2982	16158		2.07	2.6E-02	AF108906.1	NT	Chicken dorsalin-1 mRNA, complete cds
5025	16184	31131	3.99	2.6E-02	L12032.1	NT	Dinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5176	18298	31261	1.22	2.6E-02	AE002014.1	NT	xe52504.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2670383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5203	18324	31263	2.54	2.6E-02	AW241154.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6011	19195		2.94	2.6E-02	AL161683.2	NT	gg27H11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6349	18519		6.95	2.6E-02	AL206030.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6555	19717	33093	2	2.6E-02	BE521748.1	EST_HUMAN	Vaccinia virus ORF1L, strain Wyeth
6569	20194	33619	0.53	2.6E-02	Z39064.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6886	20194	33620	0.83	2.6E-02	Z88064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33520	5.63	2.6E-02	6881271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20320	33989	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8703	21783	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	al22674.s1 Soares NIH Homo sapiens cDNA clone IMAGE:1406719 3'
9560	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36841	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36842	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10814	23648	37257	5.37	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747	38547	1.59	2.6E-02	AA279351.1	EST_HUMAN	zs84402.11 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:704182 5'
11661	24849	38547	1.35	2.6E-02	AW500547.1	EST_HUMAN	UHF-BND-ak-e-10-0-UL1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3077488 5'
12490	26150	31553	1.48	2.6E-02	BF343827.1	EST_HUMAN	602015301F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4160944 5'
12583	26392		1.32	2.6E-02	11422838	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12947	25658		1.39	2.6E-02	R43678.1	EST_HUMAN	yo8807.a1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element:
545	13738	26762	1.75	2.5E-02	A1783130.1	EST_HUMAN	on26103.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
645	13738	26763	1.75	2.5E-02	A1783130.1	EST_HUMAN	on26103.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
832	14010	27068	9.54	2.6E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950685 3'
892	14088	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950685 3'
2821	15935		2.53	2.5E-02	U12671.1	NT	Rattus norvegicus ribophyllin-3A mRNA, complete cds
3021	16197	29210	2.05	2.5E-02	X93697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	29220	2.05	2.5E-02	X93697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4156	18488	30302	0.92	2.6E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-412 NN0128 Homo sapiens cDNA
4156	18488	30303	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-412 NN0128 Homo sapiens cDNA
4322	17495	30450	4.66	2.6E-02	AW582144.1	EST_HUMAN	hr36108.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5630	19021	32327	0.72	2.5E-02	A1732776.1	EST_HUMAN	z685o10.x6 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:810354 3'
6322	19494		4.88	2.5E-02	BE670128.1	EST_HUMAN	7630e09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element:
6338	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3628064 5'
6468	19633	32984	0.8	2.5E-02	L28029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
8008	21058	34570	0.84	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8167	21249	34788	0.6	2.5E-02	BE282468.1	EST_HUMAN	601108201F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	36845	0.92	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9184	22242	35785	0.57	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2616370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D.radicum 28S ribosomal RNA, D2 domain
10910	23943	37486	0.65	2.5E-02	A147615.1	EST_HUMAN	gb22a08.x1 Soares_pregnant_uterus_NH-IPU Homo sapiens cDNA clone IMAGE:1668982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A1alpha) and major histocompatibility protein class II beta chain (I1beta) genes, complete cds;
							butyrophilin-like (NG9), butyrophilin-1p
11120	24192		2.93	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12065	25046		1.87	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
12419	26072		2.17	2.6E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12621	25934		1.28	2.5E-02	11433220	NT	Dicotyledon discoidium putative protein kinase MlkaA (mikaA) gene, complete cds
12716	25476		1.83	2.5E-02	U60189.1	NT	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
12760	25497	32032	1.98	2.5E-02	BE973327.1	EST_HUMAN	bt72c07.x1 Soares_NH-IPU_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
178	13401	26431	1.44	2.4E-02	A178582.1	EST_HUMAN	yt75f11.f1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1628	14780	27865	1.89	2.4E-02	H65894.1	EST_HUMAN	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30609	1.69	2.4E-02	J06110.1	NT	T.Hamophilus calcium-binding 28 kDa (TCBP 28) protein mRNA, complete cds
6344	19514	32871	0.86	2.4E-02	W86680.1	EST_HUMAN	z163h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7370	20449	33912	1.2	2.4E-02	Z0573.1	EST_HUMAN	H5AAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7388	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7388	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21156		0.76	2.4E-02	AW819007.1	EST_HUMAN	RC3-ST0196-230300-019-H08 ST0186 Homo sapiens cDNA
8129	21211		0.57	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
							yt12c05.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:233876 3' similar to contains
8636	21716		0.57	2.4E-02	H78376.1	EST_HUMAN	Alu repetitive element; contains A3R repetitive element;
8728	21808	35344	11.69	2.4E-02	N69442.1	EST_HUMAN	z335g11.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:264596 3' similar to
9187	22285	35808	0.78	2.4E-02	AE001125.1	NT	gbK02909RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element;
							Borrelia burgdorferi (section 11 of 70) of the complete genome
							zu91c06.s1 Soares_leslie_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET
9211	22289	35831	0.81	2.4E-02	AA025660.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
							XTR repetitive element;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	38516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana mybdopterin synthase sulphuryase (csm5) gene, complete cds
9893	22933	38517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana mybdopterin synthase sulphuryase (csm5) gene, complete cds
10011	23049	38643	2.75	2.4E-02	AV692654.1	EST_HUMAN	AV692654 GK0 Homo sapiens cDNA clone GKCDSC03 5'
10186	23223	38817	2.82	2.4E-02	AA493894.1	EST_HUMAN	nt07b12 st NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:343683 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
10899	23872		0.6	2.4E-02	BE387111.1	EST_HUMAN	60127462F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815902 5'
11874	24862	38557	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III region Hsc701 gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11874	24862	38558	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III region Hsc701 gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	25163		3.08	2.4E-02	9027909	NT	Backeriphege bil67, complete genome
12362	25260	32116	4.45	2.4E-02	8763635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12478	25330	32056	1.38	2.4E-02	U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12898	25445		10.87	2.4E-02	AB008589.1	NT	cds
12897	25464		1.28	2.4E-02	N42880.1	EST_HUMAN	y908cd01.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270610 5'
12883	25900	31858	1.25	2.4E-02	AA179883.1	EST_HUMAN	zp13h01.1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608391 5'
1821	15084		5.25	2.3E-02	W05340.1	EST_HUMAN	z894g08.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288284 5'
1836	15079		16.26	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (NT6) gene, exon 4
2065	15205	28321	0.89	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-511 UM0038 Homo sapiens cDNA
2428	15564	28681	2.68	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3773	16634	28940	7.02	2.3E-02	Z29377.1	EST_HUMAN	HSAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16867		0.67	2.3E-02	L23429.1	NT	Canis beta-galactoside-binding lectin (LGALS3) mRNA, 3' end
4287	17412	30368	1.17	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4287	17412	30369	1.17	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30600	1.08	2.3E-02	AW699107.1	EST_HUMAN	CU44-NN0080-290400-160-504 NN0080 Homo sapiens cDNA
4571	17709	30689	0.8	2.3E-02	BE93225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE93225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW583683.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18468	30682	1.2	2.3E-02	AW593683.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770571 3'
4717	17852	30835	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955398 5'
4717	17852	30836	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955398 5'
5144	18267	31237	0.9	2.3E-02	AW944307.1	EST_HUMAN	RC2-CN0051-280100-011-407 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5265	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV PseF subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6365	19335	32894	0.62	2.3E-02	BF106484.1	EST_HUMAN	601822321R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042828 3'
6755	19911	33306	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.69	2.3E-02	BE141475.1	EST_HUMAN	MFR-H10080-011099-002-c08 HT0080 Homo sapiens cDNA
7619	20989	34184	-0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8060	21143	34661	4.52	2.3E-02	U63610.1	NT	Human pleckstrin (PLEK1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.76	2.3E-02	AF685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AF685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8338	22414	35967	0.84	2.3E-02	P41988	SWISSPROT	HYPOTHETICAL 55.8 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36882	1.44	2.3E-02	AE000186.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000186.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37789	2.38	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	25819		3.61	2.3E-02	BE278331.1	EST_HUMAN	60179058F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546587 5'
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043628F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043628F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12819	25604	31974	2.47	2.3E-02	U36934.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12975	26195		1.88	2.3E-02	U11077.1	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
756	13937	26982	3.59	2.2E-02	AF018287.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1786	14935		1.78	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2072	15212	26329	2.17	2.2E-02	Z32001.1	NT	S.pneumoniae popA gene and open reading frames
3621	16887		2.03	2.2E-02	AA577785.1	EST_HUMAN	m24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3738	16897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3856	17114	30116	0.88	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
4029	17185	30185	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5177	18299	31262	1.37	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7398	20474	33941	3.43	2.2E-02	AV889721.1	EST_HUMAN	AV889721 GKB Homo sapiens cDNA clone GKBAND03 3'
8568	21847	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21847	35189	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22088	35680	0.82	2.2E-02	X79468.1	NT	P. vulgata alpha tub 2 mRNA
9850	22898	36478	0.48	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9850	22898	36478	0.48	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9850	22898	36478	0.48	2.2E-02	AJ243025.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36511	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB026898.1	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
10409	23444		1.25	2.2E-02	6878140	NT	ne47m07.s1 NCI_CGAP_Cos8 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
12826	25421		6.8	2.2E-02	AA503593.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
432	13627		4.48	2.1E-02	AV761502.1	EST_HUMAN	Dicystosellum discoideum Histidine Kinase C (dhkC) mRNA, complete cds
462	13657		6.62	2.1E-02	AF029728.1	NT	Bacillus subtilis codKLM cluster, CodK (codK), and spore coat protein CotM (cotM) genes, complete cds
1202	14448	27514	6.65	2.1E-02	U72073.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27844	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27845	1.31	2.1E-02	AF204395.1	NT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28095	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28096	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28097	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28284	0.97	2.1E-02	AF190899.1	NT	Tegula aureodincta major aerosol protein precursor (TMAP) mRNA, complete cds
2092	15232	28354	1.16	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2092	15232	28355	1.16	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N28283.1	EST_HUMAN	y43h07.1 Soares melanocyte 2NHFM Homo sapiens cDNA clone IMAGE:284541 5'
3674	16837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	z65309.1 Soares fetal_fetus Nib2HFB sw Homo sapiens cDNA clone IMAGE:796121 5'
4249	17395	30384	0.68	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4427	17567	30549	0.89	2.1E-02	BF943655.1	EST_HUMAN	602016306F1 NCI_CGAP_Br64 Homo sapiens cDNA clone IMAGE:4151161 5'
4567	17705	30685	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30698	1.64	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17804	30853	5.95	2.1E-02	Y08601.1	NT	A. thaliana mitochondrial genome, part A
4852	17985	30973	0.76	2.1E-02	AA665737.1	EST_HUMAN	sg55g12.e1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	A1823432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5316	18432	31402	0.91	2.1E-02	BF026405.1	EST_HUMAN	601671411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.6	2.1E-02	AW376329.1	EST_HUMAN	CNA4-H10244-111189-040-H05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF086186.1	EST_HUMAN	QV3-GN0058-120900-328-a12 GN0058 Homo sapiens cDNA
8716	21796	35333	0.68	2.1E-02	9760238	NT	Mus musculus sorting nexin 1 (SNX1), mRNA
9703	22762	36322	0.54	2.1E-02	AA984288.1	EST_HUMAN	am83a07.a1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L26324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10268	23301	36869	0.75	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and
10558	23889	37508	0.49	2.1E-02	AF001518.1	NT	UmuD MucA homolog genes, complete cds; and unknown genes
11787	24777	38474	1.48	2.1E-02	6754255	NT	am83a07.a1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12063	25044	38762	1.42	2.1E-02	AW844320.1	EST_HUMAN	Alu repetitive element; contains element MER11 repetitive element;
12602	18493		11.16	2.1E-02	Y19213.1	NT	Bacillus halodurans genomic DNA, section 13/14
12647	26616	31862	1.22	2.1E-02	L34170.1	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp89a), mRNA
13091	25712	31898	3.82	2.1E-02	AF183913.1	NT	RCA-CN0050-130200-012-H04_1 CN0050 Homo sapiens cDNA
19	13257	26257	1.28	2.0E-02	BF002832.1	EST_HUMAN	Homo sapiens putative psbH-BA pseudogene for hair keratin, exons 2 to 7
20	13258	26258	14.96	2.0E-02	AW895665.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
269	13488	26518	5.03	2.0E-02	9753635	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
306	13622	26556	2.96	2.0E-02	AA455638.1	EST_HUMAN	MER1 repetitive element;
821	14000	27054	3.63	2.0E-02	6753635	NT	QVJ-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
1111	14276	27333	0.98	2.0E-02	AL066805.1	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1228	14366	27448	0.91	2.0E-02	8922391	NT	ser15b10.1 Soares_Nhi-HMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [1(p96.33)] of Homo sapiens
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	14386	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15055	28168	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28169	1.84	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2859	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:33089898 3' similar to contains MER1.13
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 88
3299	16473		1.89	2.0E-02	AF095888.1	NT	(Sema8b), mRNA
4113	17267	30287	1.57	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5219	18341		0.74	2.0E-02	AU71895.1	EST_HUMAN	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	q83603.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1866076 3'
7723	20787	34275	0.95	2.0E-02	AP000004.1	NT	Dicotyledonous discedium class VII unconventional myosin (myoI) gene, complete cds
7723	20787	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10081	23119		2.39	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10570	23605	37210	1.84	2.0E-02	AI640342.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
10879	23954	37592	1.65	2.0E-02	Z73968.1	NT	wt17b02.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2298315 3'
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 83/162
11978	24953	38684	2.04	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11978	24963	38685	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18409		1.8	2.0E-02	AA456538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12844	15973		2.26	2.0E-02	AL161532.2	NT	ear15b10.t1 Scores_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:513507 5'
13186	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
711	19893	26928	2.42	1.9E-02	AA572784.1	EST_HUMAN	yc04c09.t1 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:24676 5'
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	mf18a07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.11 L1
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	repetitive element
2970	18148	28164	9.15	1.9E-02	AA713856.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3018	16194	29217	1.82	1.9E-02	AV648690.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3332	16505		0.72	1.9E-02	AB039611.1	NT	nm0405.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1235337 3'
3699	16860		1.12	1.9E-02	N52250.1	EST_HUMAN	AV648690 GLC Homo sapiens cDNA clone J1.CBLH07 3'
3793	16954		8.1	1.9E-02	BE738088.1	EST_HUMAN	Utrichius talpoides mitochondrial gene for cytochrome b, complete cds
3808	16988	29971	0.83	1.9E-02	AI901183.1	EST_HUMAN	y228502.s1 Scores_multiple_polarosis_2NHRMSP Homo sapiens cDNA clone IMAGE:284331 3'
							601672882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
							q104c07.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17909	30306	1.3	1.9E-02	AF141940.1	NT	Myoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4683	17798	30785	2.79	1.9E-02	A1452898.1	EST_HUMAN	46804.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18631	31609	0.96	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5808	18097	31780	0.83	1.9E-02	AB019507.1	NT	Drosophila karekoi gene for glyceral-3-phosphate dehydrogenase, complete cds
7250	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7250	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7769	21848	36168	1.33	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 317
9632	22597	36168	1.21	1.9E-02	BF316123.1	EST_HUMAN	801896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126482 6'
9914	22854	36540	0.67	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23288	36882	1.24	1.9E-02	BF695832.1	EST_HUMAN	801852385F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076283 5'
10458	23463	37104	0.87	1.9E-02	D64001.1	NT	Synochrysis sp. PCC8803 complete genome, 2027, 2535000-2844784
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25824	31886	4.41	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament fibrin mRNA, complete cds
13008	25890		1.46	1.9E-02	L11068.1	NT	Candida albicans lambda Cas3/B fragment
356	13567	26506	1.67	1.8E-02	AW771104.1	EST_HUMAN	hm52a06.x1 NCJ_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
703	13693	26918	1.91	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1186	14348	27408	1.43	1.8E-02	X17684.1	NT	801894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1467	14821	27704	1.38	1.8E-02	AF243382.1	NT	H. fructified mRNA for myosin basic protein (MBP)
2743	15960	28972	1.74	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encora (enc) mRNA, complete cds
3282	16456		0.94	1.8E-02	A1805829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3983	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	ts52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
3983	17160	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4550	17688	30638	1.52	1.8E-02	AW896963.1	EST_HUMAN	ak2404.s1 Soares_testis_N-TT Homo sapiens cDNA clone IMAGE:1406835 3'
6068	18197	31171	2.02	1.8E-02	O60810	SWISSPROT	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
6949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
7824	20694	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7650	20694	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	801763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028280 5'
							801763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028280 5'

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8883	21743	35283	0.46	1.8E-02	AW805327.1	EST_HUMAN	Q12-NN1073-220400-159-109 NN1073 Homo sapiens cDNA
8710	21780	35328	0.76	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9683	22742	36311	0.57	1.8E-02	BF241824.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108303 5'
9683	22742	36312	0.57	1.8E-02	BF241824.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108303 5'
9842	22882		2.23	1.8E-02	AA897543.1	EST_HUMAN	q18208.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbL11672 ZINC
10268	23303	36900	1.7	1.8E-02	BE778274.1	EST_HUMAN	FINGER PROTEIN 91 (HUMAN);
10431	23466	37072	1.29	1.8E-02	X98933.1	NT	601463545F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3888863 5'
11721	23907	37530	1.78	1.8E-02	AB002337.2	NT	L signal mRNA for myomodulin neuropeptide precursor
11721	23907	37531	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	38602	1.55	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11926	24912	38613	2.45	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1169001-1495000 nt. position (87)
13096	25994		1.78	1.8E-02	AF202180.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
929	14104	27187	1.34	1.7E-02	BE394869.1	EST_HUMAN	Plasmodium falciparum erythrocyte membrane-associated plant protein antigen 332 (Ag332) gene, partial cds
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	601310826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	HS4403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
1920	15063		2.85	1.7E-02	AL163204.2	NT	L1.11 L1 repetitive element;
2161	15316		13.19	1.7E-02	AB004816.1	NT	HS4403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
2706	15823		1.38	1.7E-02	7657495	NT	Homo sapiens chromosome 21 segment HS21C004
3062	16236	29259	0.89	1.7E-02	A1147816.1	EST_HUMAN	Oryctolagus cuniculus mRNA for mitogen-activated protein kinase 20, complete cds
3602	16769		4.84	1.7E-02	AW827388.1	EST_HUMAN	Homo sapiens putative Rab5 GTP/GTP exchange factor homologous (RABEX5), mRNA
3716	16877		0.83	1.7E-02	FO4929	SWISSPROT	q622a08.x1 Soares_pregnant_uterus_NthHPU Homo sapiens cDNA clone IMAGE:1838982 3'
4284	17429		1.23	1.7E-02	AA688618.1	EST_HUMAN	hm45d04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
4317	17460		2.02	1.7E-02	RO2606.1	EST_HUMAN	MER19.b1 MER19 repetitive element;
4576	17713	30687	0.74	1.7E-02	A1305279.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	act1904.s1 Stragene ovary (#837217) Homo sapiens cDNA clone IMAGE:355927 3' similar to contains Alu
							repetitive element/contains element MER24 repetitive element;
							y66108.t1 Soares fetal liver spleen 1NFL9 Homo sapiens cDNA clone IMAGE:124847 5'
							qm08q07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gbX52359 ZINC
							FINGER PROTEIN 90 (HUMAN);
							hm4403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
							L1.11 L1 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4838	17089	30857	1.91	1.7E-02	V00941.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4834	18084		5.08	1.7E-02	AI015078.1	EST_HUMAN	ov51c02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.69	1.7E-02	A1769247.1	EST_HUMAN	wg33f09.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element
6709	19887	33256	1.23	1.7E-02	AK038280.1	EST_HUMAN	ov55h103.x1 Soares fetal_liver_splice_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7195	20080	33471	1.28	1.7E-02	AF180930.1	NT	Mus musculus protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34061	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7621	20972		1.71	1.7E-02	AI010770.1	NT	Homo sapiens hyperin gene, exons 1-50
9538	21079	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9900	22940	36526	1.28	1.7E-02	AL040554.1	EST_HUMAN	DKFZP434H314.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZP434H314.5'
12063	25073	38790	1.68	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MISE66), mRNA
12981	26111	31687	2.35	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-406 NN1030 Homo sapiens cDNA
13166	25757	31928	1.46	1.7E-02	AAB46926.1	EST_HUMAN	ce08d04.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element
524	13717		4.05	1.6E-02	AL021829.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1889	14841	27928	1.37	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologues
2323	15455	28586	1.81	1.6E-02	Q64178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28587	1.81	1.6E-02	Q64178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	15754	28669	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2708	15826	28941	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910867
2758	15876		1.01	1.6E-02	AB014634.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29768	5.33	1.6E-02	AW850662.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, topasin, RakGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17556	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-07 PT0012 Homo sapiens cDNA
5367	18570	31488	0.59	1.6E-02	AI281385.1	EST_HUMAN	q42b08.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1067417 3'
5741	18634	32234	1.42	1.6E-02	6871716	NT	Mus musculus CD6 antigen (Cd6), mRNA
6780	19636	33331	2.16	1.6E-02	AB015281.1	NT	Canidia albicans CaGCR3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027671.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.98	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.6E-02	X05151.1	NT	Human epoC-II gene for preproapolipoprotein C-II
10246	23281		2.97	1.6E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.6E-02	AA572818.1	EST_HUMAN	nt18q03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10633	23667	37277	1.61	1.6E-02	AA572818.1	EST_HUMAN	nt18q03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11149	23668	37848	2.9	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEID260 (=T1618E11))
11488	24547	38219	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24647	38220	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.6E-02	AJ373558.1	EST_HUMAN	q28b10.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12348	15455	28588	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	16343	28469	3.58	1.5E-02	N39521.1	EST_HUMAN	W27b07.s1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:243625 3'
2244	15377	28505	1.6	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3128	16304	28317	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	28318	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16978	28882	1.14	1.5E-02	AJ006216.1	EST_HUMAN	NR4-TN0115-080900-201-512 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.5E-02	BF092842.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19582	32857	2.07	1.5E-02	AF260725.1	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20547		1.69	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7561	20633	34108	1.57	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34650	1.38	1.5E-02	AL163503.2	NT	Homo sapiens chromosome 21 segment HS21C103
8058	21147	34658	3.08	1.5E-02	11417739	NT	Homo sapiens vely-fRNA synthetase 2 (VARS2), mRNA
9030	22109	36650	1.42	1.5E-02	BF345594.1	EST_HUMAN	602018135F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5'
9030	22109	36650	1.42	1.5E-02	BF345594.1	EST_HUMAN	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9030	22109	36650	1.42	1.5E-02	BF345594.1	EST_HUMAN	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22760	36537	1.59	1.5E-02	D44806.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36849	1.3	1.5E-02	R32867.1	EST_HUMAN	yf64b10.r1 Scores placenta Nb2-4P Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36850	1.3	1.5E-02	R32867.1	EST_HUMAN	yf64b10.r1 Scores placenta Nb2-4P Homo sapiens cDNA clone IMAGE:133531 5'
10650	23893	37514	0.46	1.5E-02	T92188.1	EST_HUMAN	yel17f10.s1 Strabagene lung (4937210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.5E-02	D26547.1	NT	Rice gene for flaredodin h, complete cds

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
430	13626		1.64	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC81225), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1328	14483		2.49	1.4E-02	U67778.1	NT	Xenopus laevis neurogranin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16458	29478	1.83	1.4E-02	AF160989.2	NT	Blifobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agl.) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (nagCxyR) gene, partial cds
3485	16653	28658	1.23	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3573	16738	28763	6.9	1.4E-02	AL161686.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16738	28764	6.9	1.4E-02	AL161686.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	28787	0.75	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3746	16907	28911	12.14	1.4E-02	6939918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4612	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGE resequences, MAGG Homo sapiens cDNA
4612	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGE resequences, MAGG Homo sapiens cDNA
4998	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4998	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	26210		0.74	1.4E-02	X01338.1	NT	H. sapiens LaSS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA55030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1020900 3' similar to contains Alu repetitive element
6545	19707	33084	4.52	1.4E-02	AA55030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1020900 3' similar to contains Alu repetitive element
8333	21416		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/162
9099	22178	35722	1.44	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9356	22431	35989	1.41	1.4E-02	AJ27265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22655	36227	1.66	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10780	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12268	25104	38358	8.95	1.4E-02	X00459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12840	25430		1.84	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J6.2 mRNA, complete cds
12858	25625		1.45	1.4E-02	11426868	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF23959.2	NT	Rhcam x cultorum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1913	15058		1.19	1.3E-02	BE739283.1	EST_HUMAN	601666462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21, segment HS21C001
2512	15638	28769	0.98	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 208 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602120475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602120475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4078	17292		1.22	1.3E-02	AF189288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
6276	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thiorodoxin h, complete cds
6360	18563	31478	1.61	1.3E-02	AL049888.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, mmxap28orf
6360	18563	31479	1.61	1.3E-02	AL049888.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, mmxap28orf
6293	19486	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6327	19489	32858	1.05	1.3E-02	M62862.1	NT	G. reithardii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	aw03g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8678	21768	35294	1.67	1.3E-02	AF156861.1	NT	Homo sapiens human endogenous retrovirus W gagCS.37 G gag (gag) gene, complete cds
10411	23446	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.85	1.3E-02	AE001804.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11289	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx04e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11289	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx04e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12845	26127		1.7	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2539451 to 2812870
12763	25489		2.56	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12965	25885		30.16	1.3E-02	AF162238.1	NT	Homo sapiens V1b vespressin receptor (VPR3) gene, complete cds
219	19441		0.82	1.2E-02	X87944.1	NT	H.sapiens DMA, DMB, HLA-Z1, iPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 8, 13 and 14 genes
366	19576	26606	4.38	1.2E-02	AA059238.1	EST_HUMAN	zf65g01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
495	19690	26696	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
767	19838	26983	2.67	1.2E-02	AI183522.1	EST_HUMAN	qd68a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element;
2246	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	15840	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	x37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15840	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	x37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16346		7.3	1.2E-02	AA075418.1	EST_HUMAN	zm88603.11 Stragene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:646020 5'
3359	16531	28545	2.05	1.2E-02	R62805.1	EST_HUMAN	y111508.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:198803 3'
3362	16534	28548	0.59	1.2E-02	A1686894.1	EST_HUMAN	zb86507.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
5035	18163	31139	2.02	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP13) gene, complete cds
5154	18278		1.97	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5195	18317	31286	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19061	32368	1.78	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6243	19417	32766	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbcx1 (WBSCR1) and wbcx5 (WBSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33983	1.42	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7466	20540	34014	8.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7729	20791	34280	0.66	1.2E-02	BF216850.1	EST_HUMAN	601882b49f.1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8186	21268	34792	2.3	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8321	21403	34928	0.56	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34994	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76887.1	EST_HUMAN	y172c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9839	22379	38461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus group 2 gene for capsid protein, complete cds
9872	22912	36497	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Speet gene for speeth protein
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
12974	25834		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujwre) Homo sapiens cDNA clone GEN-557G08 5'
1298	14454	27620	1.22	1.1E-02	AA070364.1	EST_HUMAN	zm88611.s1 Stragene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14882	27886	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1743	14882	27887	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2098	15236	28357	5.35	1.1E-02	BF345283.1	EST_HUMAN	602018037F.1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2942	16119		5.31	1.1E-02	N95523.1	EST_HUMAN	z140d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285040 5'
3812	16778	29792	3.59	1.1E-02	AI653508.1	EST_HUMAN	iq8b10.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2218539 3' similar to SW.XPF_HUMAN
4222	17370		0.86	1.1E-02	AW813798.1	EST_HUMAN	Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4651	18061	31057	1.27	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKF7z588E092A.s1 588 (synonym: hute1) Homo sapiens cDNA clone DKF7z588E0924
							Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynab), YnaC (ynac), YnaD (ynad), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), xylan beta-1,4-xylosidase
6277	19481	32800	0.89	1.1E-02	U69480.1	NT	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7773	20830	34321	2.19	1.1E-02	BE149811.1	EST_HUMAN	Melanogpus sanguinipes entomopoxvirus, complete genome
7909	21039	34561	1.25	1.1E-02	8631294	NT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	QV3-BN0045-220300-128-h02 BN0046 Homo sapiens cDNA
8841	21620	35458	0.89	1.1E-02	AW898180.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC-4040
9022	22101	35641	0.7	1.1E-02	C04803.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9103	22182	35727	7.44	1.1E-02	Q81982	SWISSPROT	
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	z124d01.r1 Stratiene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:549328 5'
10299	23334	36839	4.06	1.1E-02	AA314685.1	EST_HUMAN	EST188494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24293	37934	2.41	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12185	25152						ab77711.s1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
7	13245	26247	4.01	1.1E-02	AA688289.1	EST_HUMAN	Alu repetitive element
1552	14705	27785	8.82	1.0E-02	AW849120.1	EST_HUMAN	MR3-CT0176-111099-003-g10 CT0176 Homo sapiens cDNA
2638	16761		0.97	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3159	16334	28344	1.71	1.0E-02	AA068389.1	EST_HUMAN	cc22h08.s1 NCI CGAP_G031 Homo sapiens cDNA clone IMAGE:1350495 3'
3336	16509	28525	2.88	1.0E-02	BE835558.1	EST_HUMAN	RC0-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3598	16762		1.24	1.0E-02	BE989998.1	EST_HUMAN	601849987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3986	17143	30148	0.7	1.0E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 GT0060 Homo sapiens cDNA
4002	17159	30165	0.85	1.0E-02	A1065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4899	18029	31017	0.59	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4989	18098	31074	5	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5116	18243	31208	4.14	1.0E-02	R06567.1	EST_HUMAN	yc54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196833 5'
5242	18364	31332	0.83	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5632	18729	31745	1.96	1.0E-02	P06599	SWISSPROT	EXTENSIN PRECURSOR
			0.81	1.0E-02	H52681.1	EST_HUMAN	yc36h11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235941 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5865	18055	32382	0.68	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A To4 (Nfat4) gene, exons 1 and 2
6242	19416	32784	1.28	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6310	19482	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6801	20216	33846	1.68	1.0E-02	Z29842.1	NT	Z.mays U3snRNA pseudogene
8683	22848	36219	6.34	1.0E-02	BF036331.1	EST_HUMAN	601465670F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3883177 5'
8683	22848	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601465670F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3883177 5'
11542	24598		2.12	1.0E-02	AF157589.1	NT	Orithidia fasciculata 27 kDa guinea RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11573	24828		1.7	1.0E-02	A1417961.1	EST_HUMAN	ig55h07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1
11649	24728	38420	1.85	1.0E-02	AV780016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5
12278	26206		1.76	1.0E-02	Q62203	SWISSPROT	repetitive element
12339	26841	31782	3.68	1.0E-02	AW835521.1	EST_HUMAN	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12355	26902		4.31	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12764	25974		1.4	1.0E-02	AJ276505.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12849	26060		2.81	1.0E-02	X82654.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
916	14061	27156	5.69	9.0E-03	A1796126.1	EST_HUMAN	H.sapiens gene for Me497/CD63 antigen
1283	14449		1.66	9.0E-03	BE781880.1	EST_HUMAN	WH4208.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2488	15588	28721	2.64	9.0E-03	AL161592.2	NT	MER22 MER22 repetitive element
2871	16147	29185	0.81	9.0E-03	AI251744.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2871	16147	29186	0.81	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 59
3758	16819	28821	0.88	9.0E-03	J05184.1	NT	q180709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5831	18117		1.18	9.0E-03	AI809792.1	EST_HUMAN	q180709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
6768	19822		4.01	9.0E-03	BE746988.1	EST_HUMAN	S.saccharosus thermoplasma gene, complete cds
7623	20893	34168	0.61	9.0E-03	AI242219.1	EST_HUMAN	w77704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
7640	20708	34188	0.91	9.0E-03	8822570	NT	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
8059	21142		0.8	9.0E-03	AL038991.1	EST_HUMAN	q187c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853874 3'
8443	21524		0.54	9.0E-03	AF223391.1	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
10050	23088	36600	0.54	9.0E-03	P28011	SWISSPROT	DKFZp434L0412_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0412 5'
10068	23104	36707	1.47	9.0E-03	P20908	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
							COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.68	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11951	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preproglucagon (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preproglucagon (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183181 3'
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.16	8.0E-03	AAT23007.1	EST_HUMAN	zh30e03.s1 Soares_pituitary_gland_NSHPG Homo sapiens cDNA clone IMAGE:413698 3' similar to contains
1013	14185	27246	12.69	8.0E-03	AF109658.1	NT	Alu repetitive element
2226	16360	28489	1.87	8.0E-03	AL163263.2	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
2017	15741	28853	3.95	8.0E-03	P10266	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
3442	16610	28628	1.02	8.0E-03	AJ131016.1	NT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDOUCLEASE]
3768	16927	28630	1.81	8.0E-03	P32844	SWISSPROT	Homo sapiens SCL gene locus
3768	16927	28631	1.81	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE940049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4502	17642	30627	6.73	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4839	17972	30961	0.63	8.0E-03	P03181	SWISSPROT	GM4-NN0119-300800-223-b05 NN0119 Homo sapiens cDNA
4839	17972	30962	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18390	31358	0.94	8.0E-03	AU140261.1	EST_HUMAN	HYPOTHETICAL BHLF1 PROTEIN
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
6328	25823	32857	1.27	8.0E-03	AP000002.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BNG1, tapasin, RatGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	RPS18 genes, complete cds; Scam21 gene, partial
7068	20112		1.03	8.0E-03	V01109.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (277)
7357	20436	33898	1.43	8.0E-03	M17197.1	NT	PROBABLE PEPTIDASE Y4NA
7714	20779		1.8	8.0E-03	AB038267.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	A. californica (marine gastropod mollusc) neuro-peptide gene (bag cell), exon 1, 5' end
9111	22190	35734	3.53	8.0E-03	AW808692.1	EST_HUMAN	Tursiops truncatus mRNA for p40-phox, complete cds
9180	22258	35801	0.68	8.0E-03	97899561	NT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
							MP1-ST0111-111189-011-103 ST0111 Homo sapiens cDNA
							Mus musculus fusion 2 (human) (Fus2), mRNA
							QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE788441.1	EST_HUMAN	601475619f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.78	8.0E-03	Z49832.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11683	24742	38433	1.38	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11683	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24899	38701	4.37	8.0E-03	AF064598.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	25159		1.89	8.0E-03	AF68035.1	NT	Oryctolagus cuniculus cF-2a kinase mRNA, complete cds
12252	25181		7.14	8.0E-03	AB038181.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.16	8.0E-03	AI277808.1	EST_HUMAN	qir56a09.x1 Soares_placenta_6to6weeks_2Nbl-IP8x6W Homo sapiens cDNA clone IMAGE:1882762 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
999	14170	27231	3.26	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27361	3.55	7.0E-03	AV781712.1	EST_HUMAN	AV781712 HTF Homo sapiens cDNA clone HTFAZF-10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1428	14880	27653	3.39	7.0E-03	AA688298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
1632	14895	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	ab79609.s1 Stratiogene fetal retina B37202 Homo sapiens cDNA clone IMAGE:853145 3'
2332	16060	28598	2	7.0E-03	PO4929	SWISSPROT	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2695	15815		0.98	7.0E-03	AW772132.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3648	16811	28824	0.85	7.0E-03	AI150273.1	EST_HUMAN	hm57h07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032869 3' similar to contains Alu repetitive element
3663	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	qf24h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3814	17073	30071	1.13	7.0E-03	AF198344.1	NT	UIH-B18-akb-c-10-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4721	17856		0.98	7.0E-03	AW630888.1	EST_HUMAN	UIH-B18-akb-c-10-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
5103	18231		6.54	7.0E-03	AL163278.2	NT	UIH-B18-akb-c-10-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2868836 5'
5940	19126		0.72	7.0E-03	HT1108.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6238	25821		4.42	7.0E-03	AW681058.1	EST_HUMAN	yy82g01.r1 Soares_fetal_liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211824 5' similar to glcX14723 CLUSTERIN PRECURSOR (HUMAN);
6444	19811	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6567	19826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	xx33f10.r1 Soares_fetal_heart_Nrl-H19W Homo sapiens cDNA clone IMAGE:342475 5'
							EST30674 Colon I Homo sapiens cDNA 5' end

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6895	19853	33243	1.05	7.0E-03	BE657385.1	EST_HUMAN	7g34b10.x1 NCI_CGAP_Bin23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q15387
7228	20193	33550	1.93	7.0E-03	BE628133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2; contains TAR1.2 TAR1 TAR1 repetitive element;
7689	20754	34236	4.76	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7689	20754	34239	4.76	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077W
8031	21114	34632	0.59	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077W
8031	21114	34633	0.59	7.0E-03	AJ229043.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21394	34905	2.48	7.0E-03	AJ229043.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8813	21892	35433	0.58	7.0E-03	BE175667.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
8897	22652		0.84	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9794	22834	36414	0.58	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, submit II gene, complete cds; and unknown genes
9821	22861	36548	2.72	7.0E-03	P48882	SWISSPROT	y40c10.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246088 3' similar to contains
9821	22861	36549	2.72	7.0E-03	P48882	SWISSPROT	Alu repetitive element;
10513	23548		1.34	7.0E-03	AV687378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10704	23737		0.82	7.0E-03	AJ788734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10800	23833	37456	0.47	7.0E-03	BE164643.1	EST_HUMAN	AV687378 GKc Homo sapiens cDNA clone GKCAFC07 5'
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	vc37e09.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2320940 3'
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	PM3-HT0344-181189-002-p06 HT0344 Homo sapiens cDNA
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
12792	26189		1.85	7.0E-03	H64088.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12800	26534		1.46	7.0E-03	BE283253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12908	26601		1.78	7.0E-03	Y17455.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
13058	26188		1.68	7.0E-03	AL163300.2	NT	yv16h01.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
1269	14427	27494	8.78	6.0E-03	AW511148.1	EST_HUMAN	Alu repetitive element;
1269	14427	27495	8.78	6.0E-03	AW511148.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
2831	16645	28054	0.94	6.0E-03	AF112374.1	NT	Homo sapiens LSFR2 gene, penultimate exon
2956	16133	28147	3.29	6.0E-03	AA766135.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G100
2956	16133	28148	3.28	6.0E-03	AA766135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
3318	16491		2.27	6.0E-03	HT5690.1	EST_HUMAN	SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR;
							hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
							SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR;
							Danio rerio odorant receptor gene cluster
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							yv77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211551 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF190338.1	NT	Nicotian gl. cytochrome c oxidase subunit II gene, perial cds; mitochondrial gene for mitochondrial product
3468	16636	28655	1.26	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaparin reductase and vasotocin genes, complete cds
3469	16836	28656	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaparin reductase and vasotocin genes, complete cds
3636	16800		1.11	6.0E-03	W37985.1	EST_HUMAN	Z013611.1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3750	16911	28614	3.73	6.0E-03	BF510886.1	EST_HUMAN	U14-B14-apm-c-06-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17036	30034	1.31	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
4032	17188	30189	0.6	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240988-021-b10 CT0204 Homo sapiens cDNA
4067	17223		1.28	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4484	17624		1.54	6.0E-03	A0106333.1	EST_HUMAN	6036111.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17950	30635	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST127116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5305	18422	31362	0.5	6.0E-03	AA886072.1	EST_HUMAN	qf5g09.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404268 3'
6281	25822	32803	0.89	6.0E-03	9627521	NT	Varicella virus, complete genome
6956	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6994	18513	31505	0.97	6.0E-03	BE263748.1	EST_HUMAN	601112363F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7399	20477	33944	0.65	6.0E-03	AA258442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' and
7399	20477	33945	0.65	6.0E-03	AA258442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' and
7824	20879	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8042	21125	34646	6.71	6.0E-03	A033580.1	EST_HUMAN	ov13a04.x1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element:
8161	21243	34783	2.76	6.0E-03	AW789337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8236	21318		1.65	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858628 5'
9754	22692	36262	7.03	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	A432881.1	EST_HUMAN	622502.x1 NCI_CGAP_KcH11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A;
10503	23638		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fnd gene
10615	23649	37268	0.64	6.0E-03	X88398.1	NT	Homo sapiens cdc2-like acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10681	23695		0.54	6.0E-03	AF246505.1	NT	M.thermoformicum complete plasmid pFV1 DNA
10983	24082	37687	1.66	6.0E-03	AW902164.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
11049	24126		1.94	6.0E-03	11545814	NT	EST1974237 IMAGE resequences, MAGG Homo sapiens cDNA Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14566.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37838	2.86	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	25938		1.3	6.0E-03	BF871185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4282212 5'
12451	25926		4.85	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450286 (section 39 of 148) of the complete genome
12532	25933		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	26397		1.83	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12944	26822		2.41	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
13095	26018		1.61	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
13147	25746		1.19	6.0E-03	BF110298.1	EST_HUMAN	7636b11.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3'
686	13871	26903	1.69	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
688	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1136	14301	27367	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1601	14754		1.08	6.0E-03	AI138677.1	EST_HUMAN	q178d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2746	15863	26974	2.43	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	26392	3.87	5.0E-03	T87623.1	EST_HUMAN	yo81f09.s1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	6.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2NH1Bst Homo sapiens cDNA clone IMAGE:155668 3'
3351	16523		0.84	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3790	16951	28957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3854	17014	30014	0.61	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.64	5.0E-03	AA289673.1	EST_HUMAN	EST12218 Utrac tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.65	6.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4421	17562	30548	0.71	5.0E-03	HJ78355.1	EST_HUMAN	y178g10.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:240068 5'
4423	17014	30014	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17686	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

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4841	17974	30884	1.56	5.0E-03	AF52387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5288	18405		1.9	5.0E-03	4758747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6169	19345	32891	2.82	5.0E-03	O00507	SWISSPROT	
6204	19379		0.88	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6728	19882		7.34	5.0E-03	BE300081.1	EST_HUMAN	G00944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880871 3'
6986	18505	31520	7.22	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7237	20321	33765	0.61	5.0E-03	6753951	NT	Mus musculus dyx11l, exon, heavy chain 11 (Dnaxho11), mRNA
							EST03012 Fetal brain, Stragelene (cass36206) Homo sapiens cDNA clone HFB083 similar to EST containing Alu repeat
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031089-011-407 CT0255 Homo sapiens cDNA
7844	20894	34505	7.18	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8415	21498	35027	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8415	21498	35028	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8433	21514	35045	1.89	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8811	21880		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9007	22096	35829	1.21	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9140	22219	35783	0.52	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10044	23082	36884	1.03	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10176	23218	36805	0.74	5.0E-03	AW821888.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
10360	23395	37008	0.56	5.0E-03	AA533143.1	EST_HUMAN	h45h10.s1 NCI CGAP P18 Homo sapiens cDNA clone IMAGE:585587
10538	23574	37181	0.47	5.0E-03	7682567	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10696	23729		0.47	5.0E-03	AA633261.1	EST_HUMAN	ag48c10.s1 Gessier Wilms tumor Homo sapiens cDNA clone IMAGE:1128290 3'
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 684
							xn58g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element;
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	xn58g06.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element;
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	contains L1 L2 L1 repetitive element;
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	jc09e04.r1 Stragelene placenta (8937225) Homo sapiens cDNA clone IMAGE:70688 5'

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11615	24696		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2281822 5'
12070	26051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	26051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.88	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA455597.1	EST_HUMAN	z075a03.s1 Scores every tumor NIH-HOT Homo sapiens cDNA clone IMAGE:806548 3' similar to SW:DXA2_MOUSE P14985 PROBABLE DIAPHENOL OXIDASE A2 COMPONENT ;
12802	25835		5.99	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
13002	25857	31951	2.86	5.0E-03	AW449109.1	EST_HUMAN	UHLB13-4d4-08-0-U1.s1 NCI_CGAP_Sub56 Homo sapiens cDNA clone IMAGE:2734215 3'
242	13484	26463	1.54	4.0E-03	AW500186.1	EST_HUMAN	UHLF-BNO-alc-1-04-0-U1.L1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
331	13545	26575	1.75	4.0E-03	R46482.1	EST_HUMAN	UHLF-BNO-alc-1-04-0-U1.L1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:35988 3'
456	13651	26889	1.36	4.0E-03	P54675	SWISSPROT	y651e04.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:1562568 3'
616	13603	26825	4.37	4.0E-03	AA93339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	cn75g12.s1 Scores NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1562568 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	y651e04.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:510998 5'
1174	14337	27393	34.06	4.0E-03	AA069777.1	EST_HUMAN	RC3-BT0339-110100-012-017 B10333 Homo sapiens cDNA
1198	14358	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	z81a08.r1 Stragene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
1331	14488	27558	1.48	4.0E-03	AA284374.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1783	14932	28026	2.08	4.0E-03	U33472.1	NT	z559a01.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:701738 5'
2076	15215	28334	17.33	4.0E-03	AA069777.1	EST_HUMAN	Radiu norvegicus type 1 astrocyte and oligodendrocyte associated protein AT1-46 mRNA, complete cds
2321	15453		2.08	4.0E-03	BE410556.1	EST_HUMAN	z81a08.r1 Stragene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
2352	15483	28616	1.53	4.0E-03	AW794740.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838510 5'
2639	15762	28875	1.95	4.0E-03	U62111.2	NT	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28876	1.96	4.0E-03	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDMP protein (CDMP), adrenoleukodystrophy protein >
2755	15972	28980	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDMP protein (CDMP), adrenoleukodystrophy protein >
2755	15972	28981	2.97	4.0E-03	AJ277365.1	NT	CDMP protein (CDMP), adrenoleukodystrophy protein >
2761	15977	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3287	16471	29491	1.09	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens polyglutamine-containing C14ORF4 gene

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3297	16471	28492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151288-003-108 HT0340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW188428.1	EST_HUMAN	X68804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2865279 3'
3610	16783	29799	0.83	4.0E-03	AW188428.1	EST_HUMAN	X68804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2865279 3'
3714	16875	29880	0.84	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29880	0.85	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17166	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4102	17256		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
8339	18452	31420	0.98	4.0E-03	AW500547.1	EST_HUMAN	U1HF-BNO-ekj-e-10-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077486 5'
5390	18592	31584	1.68	4.0E-03	AF005859.1	NT	Drosophila melanogaster armo207 (arom207) mRNA, complete cds
5516	18713	31728	27.24	4.0E-03	AF169826.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5814	19102	32416	3.1	4.0E-03	P04196	SWISSPROT	(HFRG)
5918	19108	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp7611014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW690572.1	EST_HUMAN	hg48007.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848652 3'
8439	19608	32989	1.79	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461854 5'
8809	19983	33367	1.07	4.0E-03	AA813222.1	EST_HUMAN	g13211.61 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
6914	20228	33682	1.41	4.0E-03	U76408.1	NT	Lycopodium esculentum knotted 3 protein (TKG3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33496	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33689	3.73	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7588	20660	34136	0.86	4.0E-03	AJ081483.1	EST_HUMAN	bc37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20682	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7631502.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7683	20758		0.85	4.0E-03	X92108.1	NT	H.sapiens hspX gene
8128	21210	34731			Q8T192	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAM-TS-5) (ADAM-TS5) (AGGREGANASE-2) (ADMP-2) (ADAM-TS 11)
8238	21320	34838	4.61	4.0E-03	AF111944.1	NT	Dicotyledonous dicotyledon AX4 development protein DG1122 (DG1122) gene, partial cds
8308	21479	35008	2	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8695	21745	35284	0.87	4.0E-03	AF139827.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
8761	21840	35381	0.51	4.0E-03	Y12855.1	NT	Homo sapiens P2X7 gene, exon 12 and 13
8911	21980	35529	7.06	4.0E-03	A1553983.1	EST_HUMAN	bc48b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
9090	22169		3.24	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.76	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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9825	22855	38447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22855	38448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23180	38768	0.63	4.0E-03	H30864.1	EST_HUMAN	yp42g12.1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37229	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
11283	24349	37988	1.36	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-epitot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		5.84	4.0E-03	BE15173.1	EST_HUMAN	PM4-BN0138-180600-002-108 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE268280.1	EST_HUMAN	601118184F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12541	25357		1.95	4.0E-03	AW504273.1	EST_HUMAN	UIHF-BN0-ab-g-04-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3090322 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element/contains element MER31 repetitive element;
12858	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	1H02007.x1 NCL_CGAP_KM11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR6 repetitive element;
12871	25581		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-R03 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436885	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
382	13590	26828	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
802	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1894	14848	27930	3.65	3.0E-03	AA468110.1	EST_HUMAN	nc79c05.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element
2367	15498		6.37	3.0E-03	Z32521.1	NT	S.cerevisiae (cv. H10) mRNA for triosephosphate isomerase
2368	15498	28824	1.14	3.0E-03	U46898.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15498	28825	1.14	3.0E-03	U46898.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3056	16232		0.77	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoMt gene
3162	16327	28338	3.55	3.0E-03	BE378296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3220	16394	29405	2.63	3.0E-03	AW802687.1	EST_HUMAN	IL2-LIM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3504	16871	29681	2.16	3.0E-03	U24606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3513	16879		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17289	30291	1.67	3.0E-03	AF792278.1	EST_HUMAN	af04009.y5 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4641	17777	30758	4.62	3.0E-03	AF598141.1	EST_HUMAN	ju8.P10.H3 contorm Homo sapiens cDNA 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4858	17881	30978	0.88	3.0E-03	AL118087.1	EST_HUMAN	DKFZp781B0712.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B0712.5
4855	18085	31061	2.05	3.0E-03	AJ732754.1	EST_HUMAN	ab18a08.x5 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:841142.3 similar to contains Alu repetitive element
4878	18107	31083	5.53	3.0E-03	BE787846.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483.5
5255	18375	31341	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5255	18375	31342	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5262	18381	31347	1.76	3.0E-03	AI193880.1	EST_HUMAN	q880b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745275.3 similar to SW/AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17, contains MSR1.2 MER22 repetitive element
5390	18582	31451	3.38	3.0E-03	8922469	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32163	1.08	3.0E-03	AJ249881.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6883	19841	33231	0.72	3.0E-03	AA456701.1	EST_HUMAN	aa1310.r1 Soares_NHRIMP4_S1 Homo sapiens cDNA clone IMAGE:813163.5
7168	20301	33744	0.75	3.0E-03	D37877.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7354	20433	33865	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcp3 gene for purine-cytosine permease
7681	20756	34241	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8124	21206	34728	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCQ-BT0812-250800-032-e07 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCQ-BT0812-250800-032-e07 BT0812 Homo sapiens cDNA
8340	21431	34955	1.4	3.0E-03	N92580.1	EST_HUMAN	z527504.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783.3
8480	21571	35108	0.47	3.0E-03	AI866028.1	EST_HUMAN	w24409.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425841.3
8510	21691		0.63	3.0E-03	M83468.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35278	1.34	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8678	21759	35285	1.6	3.0E-03	AL163289.2	NT	Homo sapiens chromosome 21 segment HS21C068
8786	21885		1.45	3.0E-03	Q8QIM91	SWISSPROT	NONSTRUCTURAL PROTEIN V
9182	22270		10.8	3.0E-03	AW618774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2869131.3 similar to contains L1.f1 L1 repetitive element
9245	22322	35866	4.26	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9259	22345	35896	0.88	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1836247.3 similar to gb:U57138.mat
9280	22356	35908	0.53	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN)
9609	22584		0.78	3.0E-03	D80801.1	NT	602035980FT NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4188938.5
9848	21089	34804	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9856	22876		0.56	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9908	22948		6.61	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (GS)
							RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE];
10099	23137	36738	2.31	3.0E-03	P11369	SWISSPROT	ENDONUCLEASE
10200	23237	36827	1.44	3.0E-03	P51969	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2/A1)
10344	23379	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11065	24159		2.67	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20766	34241	1.45	3.0E-03	AB021738.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38457	2.52	3.0E-03	AF084481.1	NT	Homo sapiens tritucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24782	38458	2.62	3.0E-03	AF094481.1	NT	Homo sapiens tritucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
							RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE];
11848	24838	38532	1.36	3.0E-03	P11369	SWISSPROT	ENDONUCLEASE
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	UIH-B12-eth-d-08-0-UJ.s1 NCI_QGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
12198	25948		1.62	3.0E-03	AJ525056.1	EST_HUMAN	primate-6.E07.r bvtumor Homo sapiens cDNA 5'
							contains L1.03 MER26 repetitive element;
12235	26179	38348	1.24	3.0E-03	AA983154.1	EST_HUMAN	077010.s1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1822779 3' similar to
12296	26090		1.76	3.0E-03	AB009688.1	NT	contains L1.03 MER26 repetitive element;
12481	26333	32057	1.23	3.0E-03	AJ286282.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	RING CANAL PROTEIN (KELCH PROTEIN)
1304	14548	27624	2.08	2.0E-03	M20783.1	NT	Yd15h03.t1 Scores: fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1397	14551	27628	1.42	2.0E-03	AA681605.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1406	14580	27634	20.85	2.0E-03	AF284446.1	NT	nu88901.s1 NCI_QGAP_Av1 Homo sapiens cDNA clone IMAGE:1217593
							Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.28	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14698	27777	2.28	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 6(M) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA450138.1	EST_HUMAN	zxc2a10.t1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.08	2.0E-03	BE144908.1	EST_HUMAN	CMZ-HT10183-061069-018-d03 HT10183 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15468	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
2947	15770		4.93	2.0E-03	AW137782.1	EST_HUMAN	UH-HB1-adj-g-10-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16070	28680	4.92	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares_tadl_fetus_Nb2HFB_pw Homo sapiens cDNA clone IMAGE:789114 5'
3510	16676	28688	0.96	2.0E-03	BF308953.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3768	16917	28919	5.48	2.0E-03	XB7344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING3, 9, 13 and 14 genes
4062	17218	30226	0.62	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17376	30384	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP32; COAT PROTEIN GP36]
4280	17435	30423	1.02	2.0E-03	AA179683.1	EST_HUMAN	zp13M01.r1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:608361 5'
4336	17479		13.93	2.0E-03	U08491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17670		1.99	2.0E-03	L35078.1	NT	Parvovirus major outer capsid protein (VP7) mRNA, complete cds
4547	17685		1.22	2.0E-03	AW297380.1	EST_HUMAN	UH-HBW-adj-g-03-0-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17689	30670	1.05	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4698	17803	30780	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4698	17803	30781	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17991	30849	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4832	17995		1.57	2.0E-03	R87773.1	EST_HUMAN	yc45e02.s1 Soares adult brain N2b-4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4952	18091	31037	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003528.1	NT	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18796	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104682 5'
5745	25810	32238	1.83	2.0E-03	AB014568.1	NT	Homo sapiens mRNA for KIAA0893 protein, partial cds
5828	19019	32325	2.08	2.0E-03	U03711.1	NT	Xenopus laevis xellin mRNA, complete cds
6236	19411	32758	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6238	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19843	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6476	19843	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6478	19845	33007	7.65	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19879	33049	2.10	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19880	33050	0.75	2.0E-03	AV706075.1	EST_HUMAN	AV706075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6544	19708	33082	1.45	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6736	19892		1.36	2.0E-03	A1901089.1	EST_HUMAN	wu30109.x1 Soares_Diedgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to
6775	19930	33326	0.7	2.0E-03	A4677831.1	EST_HUMAN	SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ;
7088	18525	31517	1.35	2.0E-03	A3038502.1	NT	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7231	20136	33554	3.3	2.0E-03	BE067986.1	EST_HUMAN	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7294	20376	33833	0.65	2.0E-03	A1298883.1	EST_HUMAN	OM4-BT0366-061289-054-d01 BT0366 Homo sapiens cDNA
7444	20521	33894	0.8	2.0E-03	T86593.1	EST_HUMAN	gm93d11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:186885 3'
7794	20660	34342	1.41	2.0E-03	P07354	SWISSPROT	y477g10.t1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8412	21463	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	H37503.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR-Q60976
8412	21463	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	Q60976 JERKY. ;
8459	21540	35069	0.84	2.0E-03	Q92350	SWISSPROT	y42g06.s1 Soares_melanocyte_2Nblm_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains
8481	21562	35097	1.09	2.0E-03	P19137	SWISSPROT	L1.b2 L1 repetitive element ;
8536	21617	35153	1.04	2.0E-03	6005855	NT	y42g06.s1 Soares_melanocyte_2Nblm_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains
8536	21617	35154	1.04	2.0E-03	6005855	NT	L1.b2 L1 repetitive element ;
8561	21642	35161	1.03	2.0E-03	AU136879.1	EST_HUMAN	HYPOTHETICAL 32.8 KD PROTEIN C8G9.05 IN CHROMOSOME 1
8614	21694		0.9	2.0E-03	AJ400877.1	NT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
9396	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
9396	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
9441	22515	36079	1.07	2.0E-03	AF224689.1	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
9726	22791	36362	0.71	2.0E-03	H50832.1	EST_HUMAN	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
9726	22791	36363	0.71	2.0E-03	H50832.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17
9758	22696	36264	3.33	2.0E-03	P24821	SWISSPROT	gene
9868	22908	36493	1.22	2.0E-03	P46962	SWISSPROT	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9868	22908	36494	1.22	2.0E-03	P46962	SWISSPROT	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9824	22984	36552	0.6	2.0E-03	AF097732.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
							y28a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
							y28a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
							TEVASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI)
							(MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-
							225) (TEVASCIN-C) (TN-C)
							BETA-GALACTOSIDASE PRECURSOR (LACTASE)
							BETA-GALACTOSIDASE PRECURSOR (LACTASE)
							Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8624	22894	38553	0.6	2.0E-03	AF09732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	38755	0.96	2.0E-03	AW884289.1	EST_HUMAN	QV9-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
10249	23283		8.26	2.0E-03	AA251376.1	EST_HUMAN	zs10a08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3'
10628	23602	37270		2.0E-03	BF367386.1	EST_HUMAN	MR2-CN0030-140800-001-e05 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	MB9524.1	NT	Human dystrophin gene
11778	20850	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN)(LP)
11836	24825		2.98	2.0E-03	BF330808.1	EST_HUMAN	RC9-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11844	24833	38528	9.84	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	AB25745.1	EST_HUMAN	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
12188	25159	38833	4.31	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
12222	25171	38836	1.71	2.0E-03	AB84325.1	EST_HUMAN	oy45g.08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to
12245	18497		4.86	2.0E-03	AJ245187.1	NT	TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12462	26140		4	2.0E-03	AV697968.1	EST_HUMAN	Carnielus diomedentis cvhp19 gene for immunoglobulin heavy chain variable region
12661	25383	32039	1.29	2.0E-03	Y00508.1	NT	AV697968 GKC Homo sapiens cDNA clone GKCGX005 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT5, G8b, GSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13090	25927		2.48	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCGX005 5'
452	13648	26084	1.38	1.0E-03	H89471.1	EST_HUMAN	y88c08.l1 Soares_pituitary_gland_N31-PCG Homo sapiens cDNA clone IMAGE:232334 5'
852	14028	27091	1.55	1.0E-03	AI720283.1	EST_HUMAN	as701b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
852	14028	27092	1.55	1.0E-03	AI720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
1119	14284	27339	2.61	1.0E-03	AI865788.1	EST_HUMAN	as701b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1139	14304	27360	1.61	1.0E-03	AB94572.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
1192	14354	27412	0.85	1.0E-03	AI892016.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
2084	15224	28348	3.42	1.0E-03	P47803	SWISSPROT	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
2222	15356	28488	9.62	1.0E-03	AJ131016.1	NT	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
3044	16220	28241	1.37	1.0E-03	AB033117.1	NT	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
3280	16434	28451	2.81	1.0E-03	P18915	SWISSPROT	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3280	16434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3632	16786	29813	0.94	1.0E-03	U68061.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16786	29814	0.94	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
4034	17190	30200	0.88	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4044	17200	30211	0.91	1.0E-03	Z49849.1	NT	contains TAR1.11 TAR1 repetitive element:
4566	17694	30673	2.34	1.0E-03	BE839162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4588	17735	30715	4.89	1.0E-03	BE246538.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4785	17920	30808	0.81	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31050	2.54	1.0E-03	A073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840262 3'
4945	18075	31051	2.54	1.0E-03	A073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840262 3'
4946	18076		6	1.0E-03	BE164067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	hw5102.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176955 3'
5423	18624	31600	2	1.0E-03	AA280951.1	EST_HUMAN	ze4480.1.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5572	18768	31809	1.84	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.84	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5680	18894	32176	0.85	1.0E-03	BE798491.1	EST_HUMAN	601589841F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943954 5'
5686	18890	32181	1.77	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	yo07008.11 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yo07008.11 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
6033	19216		0.59	1.0E-03	BF541039.1	EST_HUMAN	602068042F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:4068907 5'
6144	19322		2.75	1.0E-03	X07698.1	NT	Mouse nucleolin gene
6184	19390	32708	0.85	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3875693 3'
6321	19493		8.77	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19631	32892	1.11	1.0E-03	T87761.1	EST_HUMAN	yo83a11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5'
6538	19702		1.68	1.0E-03	AW602585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6896	20046	33455	1.41	1.0E-03	L7570.1	NT	Homo sapiens DICGeorge syndrome critical region, centromeric and
7302	20384	33843	2.81	1.0E-03	D16828.1	NT	Human gene for fourth somatostatin receptor subtype
7656	20724		1.12	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7817	20872	34370	1.98	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7885	20937	34443	3.44	1.0E-03	M63376.1	NT	601491081F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3893276 5'
7934	20984	34492	0.79	1.0E-03	BE88044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8073	21155	34674	0.66	1.0E-03	AF274581.1	NT	Homo sapiens partial stefin-1 gene
8136	21218	34739	5.02	1.0E-03	AJ251973.1	NT	2497c09.v1 Soares_pregnant_uterus_Nb4-PU Homo sapiens cDNA clone IMAGE:460768 3' similar to
8337	21418	34944	1.95	1.0E-03	AA122770.1	EST_HUMAN	contains L1.1 L1 repetitive element;
8438	21519	35048	2.85	1.0E-03	AF163080.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8825	21705	35241	0.75	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9144	22223		1.48	1.0E-03	Y11204.1	NT	V-cardin gene encoding vchocapsin
9170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-407 LT0079 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9281	22357		0.65	1.0E-03	U62111.2	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9319	22395	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
							gtx401.x1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846673 3' similar to
9798	22836		0.47	1.0E-03	AJ247482.1	EST_HUMAN	gtx401.x1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846673 3' similar to
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
							BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE
10025	23083	36660	0.86	1.0E-03	Q01128	SWISSPROT	PROTEOGLYCAN-II) (DSPG)
10368	23401	37012	9.37	1.0E-03	AF005529.1	NT	Homo sapiens glycican 3 (GP-C3) gene, partial cds and flanking repeat regions
10372	23407		0.75	1.0E-03	AF037485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
							077908.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643176 3' similar to contains MER39.b1
10522	23557	37165	1.08	1.0E-03	A024350.1	EST_HUMAN	MER39 MER39 repetitive element;
10823	23856	37478	0.5	1.0E-03	AE004762.1	NT	Pseudomonas aeruginosa PAO1, section 323 of the complete genome
10823	23856	37479	0.5	1.0E-03	AE004762.1	NT	Pseudomonas aeruginosa PAO1, section 323 of the complete genome

Table 4

Single Exon Probes Expressed in Placenta

Probe ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10830	23863		0.53	1.0E-03	AA706202.1	EST_HUMAN	ag83f12.x1 Stratagene HNT neuron (#637233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element
10902	23866	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RG1-CT0278-181089-011-a08 CT0278 Homo sapiens cDNA
10902	23866	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181089-011-a09 CT0278 Homo sapiens cDNA
10969	24068	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
							tt73e12.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TR:Q26195 Q26195 PVA1 GENE:
11062	24138		2.03	1.0E-03	AI583847.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11426	24488		2.63	1.0E-03	AV759949.1	EST_HUMAN	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT BINDING ACTIVITY)
11924	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	(TRANSCRIPTION FACTOR NTF-1)
							(PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT BINDING ACTIVITY)
11824	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	(TRANSCRIPTION FACTOR NTF-1)
12176	25136	38831	5.51	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
							tc05h11.x1 NCI CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12679	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	Nicotiana tabacum chloroplast, complete genome
12889	26590		1.17	1.0E-03	11465934	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5327	18440	31409	0.7	9.0E-04	P08548	SWISSPROT	APOLPOPROTEIN A-IV PRECURSOR (APO-AIV)
5759	18989		2.08	9.0E-04	P06727	SWISSPROT	Homo sapiens KVLQ11 gene
6386	19557		0.58	9.0E-04	AI006345.1	NT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
6815	19775	33186	1.27	9.0E-04	P02381	SWISSPROT	Glycyrhiza glabra GgPAS1 mRNA for beta-amylin synthase, complete cds
9843	22883		1.46	9.0E-04	AB037203.1	NT	X.laevis mRNA for O4SR protein
1517	14670		1.07	8.0E-04	X08469.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4298	17439		4.4	8.0E-04	P08547	SWISSPROT	Homo sapiens prion protein (PrP) gene, complete cds
4837	18017	31002	2.5	8.0E-04	U29185.1	NT	z724c10.s1 Soares_fetal_heart_NBH119W Homo sapiens cDNA clone IMAGE:377874 3'
11412	24473		2.59	8.0E-04	AA777084.1	EST_HUMAN	tr55a08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
11576	24631		1.87	8.0E-04	AI571089.1	EST_HUMAN	Homo sapiens CYP17 gene, 5' and
1874	16018	28127	1.11	7.0E-04	L41825.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2472	15599	28724	1.45	7.0E-04	U29185.1	NT	Homo sapiens chromosome 21 segment HS21C010
2778	15894	28004	1.33	7.0E-04	AL163210.2	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3353	16525	28540	1.4	7.0E-04	4885170	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6221	18398	32745	0.93	7.0E-04	AA518212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element:
6842	18801		2.33	7.0E-04	A1768331.1	EST_HUMAN	wg3508.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7376	20455		0.72	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24883		1.7	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11863	24881	38578	3.76	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12723	25451		9.28	7.0E-04	BE077941.1	EST_HUMAN	GM1-BT0814-110300-142-b12 BT0814 Homo sapiens cDNA
13001	25630		2.68	7.0E-04	R17336.1	EST_HUMAN	y913c08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
13038	25682		5.43	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2760	15876		0.97	6.0E-04	BF341380.1	EST_HUMAN	602013339.F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4146287 5'
4069	17225	30232	1.64	6.0E-04	A1862525.1	EST_HUMAN	wf13a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4201	17350	30341	0.95	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region
4201	17350	30342	0.95	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region
4301	17444	30430	3.91	6.0E-04	U45883.1	NT	Homo sapiens COR8 chemokine receptor (CMK8RB) gene, complete cds
4665	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-009 HT0560 Homo sapiens cDNA
4665	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-009 HT0560 Homo sapiens cDNA
8050	21133		4.68	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8205	21287		0.51	6.0E-04	H82847.1	EST_HUMAN	y94a11.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231856 3' similar to contains LOR1 repetitive element:
10165	23222		3.28	6.0E-04	AL048507.2	EST_HUMAN	DKFZp566M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp566M2024
10215	23261		0.53	6.0E-04	A1858286.1	EST_HUMAN	w35g02.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2426830 3'
10285	23320	36822	2.29	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10547	23582		0.84	6.0E-04	AF287478.1	NT	Lycichnus variegatus embryonic blastocellular extracellular matrix protein precursor (ECM3) mRNA, complete cds
11774	24766	38462	2.07	6.0E-04	AJ28042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11868	24864	38540	2.47	6.0E-04	AW013947.1	EST_HUMAN	UH-B10-eab-e-09-QJL.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11937	24923		1.62	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM22-M2) (P18)
12363	26007		3.31	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0289-261199-012-d08 HT0289 Homo sapiens cDNA
13228	25797		14.14	6.0E-04	A1817088.1	EST_HUMAN	wf79g11.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element:
668	13854	26882	7.86	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1531	14884		2.03	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021069-030-007 CT0225 Homo sapiens cDNA
3500	16667	28677	1.6	5.0E-04	AA548831.1	EST_HUMAN	nt27411.s1 NCI_CGAP_C0d11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16669	28672	0.94	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6765	19821	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	z033b08.t1 Stragene colon (#637204) Homo sapiens cDNA clone IMAGE:588663 5'
7534	20507	34062	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8143	21225	34745	5.58	5.0E-04	A1185382.1	EST_HUMAN	q013f06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8498	21579	36115	0.95	5.0E-04	AA814519.1	EST_HUMAN	c086a02.s1 NCI_CGAP_C0B1 Homo sapiens cDNA clone IMAGE:1330226 3' similar to contains element MER22 repetitive element
9477	22534	36098	1.67	5.0E-04	AA846545.1	EST_HUMAN	ef56f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9571	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	KK2746F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2746 5' similar to REPETITIVE ELEMENT
9718	22763	36354	0.64	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
9809	22843	36428	4.78	5.0E-04	AW270898.1	EST_HUMAN	xs08a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768688 3'
10484	23519		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (S1M2) gene, complete cds
11220	24289		1.9	5.0E-04	AL048607.2	EST_HUMAN	DKFZp386M2024_J1 936 (synonym: hater) Homo sapiens cDNA clone DKFZp386M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA588513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12872	26961		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.76	4.0E-04	BF241482.1	EST_HUMAN	601876834F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104887 5'
680	13874	26807	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 183 of the complete genome
870	14046	27111	1.55	4.0E-04	A1720263.1	EST_HUMAN	es70b08.x1 Barcode colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334038 3' similar to TRCQ13825
870	14046	27112	1.55	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOL-COA HYDRATASE ;
1463	14646	27728	5.68	4.0E-04	AW753356.1	EST_HUMAN	es70b08.x1 Barcode colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRCQ13825
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	RCS-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							DKFZp34D059_r1 494 (synonym: hies3) Homo sapiens cDNA clone DKFZp34D059 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28827	2.04	4.0E-04	Q8816	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	18407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3387	16507	29583	0.89	4.0E-04	AF20263.1	EST_HUMAN	aa70608.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
3443	16811	29629	0.6	4.0E-04	AF69624.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE-1
4443	17583	30561	3.24	4.0E-04	AA576331.1	EST_HUMAN	AV696824 GK0 Homo sapiens cDNA clone GKCFH07 5'
4443	17583	30562	3.24	4.0E-04	AA576331.1	EST_HUMAN	nt10a10.s1 NCL CGAP_Cot1 Homo sapiens cDNA clone IMAGE:551830 3' similar to gb:M21121 T-CELL
4689	17765	30781	2.33	4.0E-04	AA088324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5199	18320	31289	3.82	4.0E-04	BE560680.1	EST_HUMAN	nt10a10.s1 NCL CGAP_Cot1 Homo sapiens cDNA clone IMAGE:551830 3' similar to gb:M21121 T-CELL
7418	20486	33965	1.55	4.0E-04	P49442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (GASR) (PARATHYROID CELL
7705	20770	34468	0.85	4.0E-04	AL161586.2	NT	CALCIUM-SENSING RECEPTOR
7896	20948	34468	0.8	4.0E-04	AU122079.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8733	21813	35348	3.84	4.0E-04	BF240712.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001820 5'
8741	21820	35354	1.08	4.0E-04	N25507.1	EST_HUMAN	60187685F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098700 5'
8892	22832	36515	3.37	4.0E-04	AI026686.1	EST_HUMAN	yc39e12.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:264142 5'
10045	23083		1.12	4.0E-04	AF022855.1	NT	oa87h03.s1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:1844341 3'
12681	25908		1.56	4.0E-04	AF254822.1	NT	Mus musculus neuropilin-2 (a17) mRNA, alternatively spliced, complete cds
180	13385	26415	9.21	3.0E-04	AL119426.1	EST_HUMAN	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
803	14078	27144	1.63	3.0E-04	U83981.1	NT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1888	16030	28137	1.7	3.0E-04	AU282100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1901	15044		0.97	3.0E-04	AI398874.1	EST_HUMAN	q228003.y1 NCL CGAP_Kdh11 Homo sapiens cDNA clone IMAGE:2028197 5'
3383	16554	29588	4.35	3.0E-04	P26147	SWISSPROT	h23a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
4071	17317	30234	4.94	3.0E-04	P49448	SWISSPROT	INTERNALIN B PRECURSOR
4187	17317		1.36	3.0E-04	AJ271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4205	17354		1.09	3.0E-04	BE140009.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4635	17771		1.16	3.0E-04	BE148548.1	EST_HUMAN	RC0-H70014-310500-028 HT0014 Homo sapiens cDNA
4637	18067		5.2	3.0E-04	BE153778.1	EST_HUMAN	MRO-HT0241-030200-008-e01 HT0241 Homo sapiens cDNA
5004	18133	31107	0.65	3.0E-04	AW687723.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
6271	19445		5.56	3.0E-04	AL163281.2	NT	QV5-D70045-221289-048-d08 DT0045 Homo sapiens cDNA
6869	20187	33611	1.54	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C081
							Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.57	3.0E-04	AW893981.1	EST_HUMAN	RC4-NN027-080400-011-008 NN027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35085	2.16	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23162	36760	1.26	3.0E-04	AA454055.1	EST_HUMAN	z448408.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M82762
10381	23416	37025	0.46	3.0E-04	AJ892139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w476a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.96	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.g1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.t1 NCI_QGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12249	26184	31555	2.39	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12846	25987	31769	2.54	3.0E-04	AB018292.1	NT	DKFZp547L195.t1 547 (synonym: tfr1) Homo sapiens cDNA clone DKFZp547L195 5'
13114	26727		4.81	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
180	13403	26432	1.33	2.0E-04	AF217798.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
491	13683	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	Human dystrrophin gene
830	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrrophin gene
830	14105	27169	5.02	2.0E-04	M86524.1	NT	Human dystrrophin gene
1206	14968		2.78	2.0E-04	AJ286021.1	EST_HUMAN	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1213	14974		2.5	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1879	15023		1.71	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Ptd3 gene
2257	15380		1.21	2.0E-04	AA476980.1	EST_HUMAN	zu33b006.e1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Abi repetitive element;
2841	15764	28878	6.42	2.0E-04	U88091.1	NT	Human gamma T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV18S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ191, TCRBJ192>
3052	16228	28248	1.23	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3'
3415	16584	29800	0.82	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3622	16988	29697	2.56	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
4022	17178	30187	0.98	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4261	17406		5.5	2.0E-04	U01029.1	NT	Phasodius vulgaris nitrate reductase (PVNR2) gene, complete cds
4791	17926	30914	1.75	2.0E-04	H98295.1	EST_HUMAN	y001e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17926	30915	1.75	2.0E-04	H98295.1	EST_HUMAN	y001e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	18048		1.22	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31256	1.47	2.0E-04	AB037897.1	NT	Danio rerio hagerman gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF057019.1	NT	Dicotyledon discoidium Interaphin (abpD) gene, complete cds
5601	18653	32136	1.11	2.0E-04	AY654362.1	EST_HUMAN	AV654362 GLC Homo sapiens cDNA clone GLC01H10.3
5674	18668	32154	1.63	2.0E-04	AI600662.1	EST_HUMAN	h03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207708.3
5688	19058	32365	0.93	2.0E-04	AA206632.1	EST_HUMAN	EST111191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
6068	19250	32678	0.92	2.0E-04	AF140708.1	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6368	19338	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AL121712.1	EST_HUMAN	AL121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798.5
7478	20553		0.84	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7798	20854		13.68	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7808	20853	34357	1.45	2.0E-04	P84286	SWISSPROT	ASSOCIATED PROTEIN
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35094	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35363	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8941	22020	35561	0.57	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
8935	22800	36173	0.58	2.0E-04	AA725700.1	EST_HUMAN	a12a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518.3
8818	22874	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLG28.1
10180	23217	36808	1.16	2.0E-04	BE146803.1	EST_HUMAN	RC3-HT0254-151059-011-505 HT0254 Homo sapiens cDNA
10223	23259	36847	2.05	2.0E-04	AA405777.1	EST_HUMAN	z163c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964.5
11088	24162	37788	3.83	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA401.5
							i01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269.3 similar to contains Alu repetitive element
11585	24638	38318	2.89	2.0E-04	AA40282.1	EST_HUMAN	element
11710	24750	38443	2.39	2.0E-04	AW136740.1	EST_HUMAN	UHF-B11-edm-c-04-OJL1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717160.3
11859	24847		2.71	2.0E-04	BE065781.1	EST_HUMAN	RC2-BT0317-150200-011-104 BT0317 Homo sapiens cDNA
12106	25086	38780	32.04	2.0E-04	P21733	SWISSPROT	HYPOTHETICAL 28.1 KD PROTEIN IN CRYB1 5'REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L18248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	26179		1.29	2.0E-04	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
788	13067	27018	0.96	1.0E-04	H89646.1	EST_HUMAN	y28c09.s1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:282884 3' similar to contains L1.1 L1 repetitive element;
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
1100	14266	27322	2.86	1.0E-04	P11369	SWISSPROT	UHH-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27358	3.79	1.0E-04	AW013847.1	EST_HUMAN	UHH-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	UHH-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62918.1	NT	Anguilla anguilla dopaminergic D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatidylinositol 3-kinase, and LAMP (LAMP) genes, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatidylinositol 3-kinase, and LAMP (LAMP) genes, complete cds
1657	14810	27895	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatidylinositol 3-kinase, and LAMP (LAMP) genes, complete cds
1808	15082	28164	2.02	1.0E-04	AB048942.1	NT	Equus caballus DNA, chromosome 2q14, microsatellite TKY38
2752	15898	28978	1.06	1.0E-04	BE218633.1	EST_HUMAN	h445c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
2752	15899	28979	1.08	1.0E-04	BE218633.1	EST_HUMAN	h445c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
3356	16528	29543	1.18	1.0E-04	Q62203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3828	16989	29902	0.86	1.0E-04	AJ440282.1	EST_HUMAN	h01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element.
4171	17321	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV847727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLC8BD04 3'
5207	18328	31288	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31289	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19166	32486	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	hcd02612.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:252
							h256d04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:383486 3' similar to gb-M67262
6977	20205	33633	0.88	1.0E-04	AA594581.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element
7336	20417	33878	12.52	1.0E-04	AJ251980.1	EST_HUMAN	q67d10.x1 NCI_CGAP_Ox2 Homo sapiens cDNA clone IMAGE:1985683 3'
7744	20417	33878	13.49	1.0E-04	AJ251980.1	EST_HUMAN	q67d10.x1 NCI_CGAP_Ox2 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21268	34789	1.02	1.0E-04	AA630453.1	EST_HUMAN	ab94p05.s1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:854654 3'
9538	22603	36175	2.75	1.0E-04	AJ806220.1	EST_HUMAN	w28a08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9548	22613	36182	1.54	1.0E-04	O68999	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9625	22680		0.76	1.0E-04	T77153.1	EST_HUMAN	yf72c08.l1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
9846	22886	36486	1.06	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23908	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24673		2.3	1.0E-04	M28537.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11650	24636	38637	1.81	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11981	24976	38680	1.94	1.0E-04	AW269061.1	EST_HUMAN	xx49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13898	26836	2.44	9.0E-05	AA718933.1	EST_HUMAN	ef45c11.x1 Soares_testes_NHT Homo sapiens cDNA clone 1282468 3'
4198	17346	30338	1.13	9.0E-05	AF762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MIER6.11
6084	19263	32595	1.37	9.0E-05	Q60716	SWISSPROT	MIER6 repetitive element;
7751	20811	34307	2.44	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	UIH-B1-ear-4-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9877	22639		3.03	9.0E-05	D86806.1	NT	UIH-B1-ear-4-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9879	22841	38211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens gene for cholesterylolign type-A receptor, complete cds
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-OpG binding protein 1 (MBD1) gene, exon 15b
11518	24574	38251	1.61	9.0E-05	AL287878.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
11916	19266	32595	3.41	9.0E-05	Q60716	SWISSPROT	repetitive element;
							q123f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
							MIR repetitive element;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12468	28016		3.37	9.0E-05	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DD4H, G8b, G8c, G8d, G8e, G8f, BAT5, G5b,
844	14022	27080	1.22	8.0E-05	AJ251646.1	NT	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
887	14063		3.11	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
9015	16191		1.01	8.0E-05	M83575.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4604	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
8948	22027	35568	0.51	8.0E-05	Y11668.1	NT	wy78a04.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
11419	24480	38146	2.58	8.0E-05	M89197.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
							Human hemoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13169	26001		1.78	8.0E-05	AA276333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
357	13688	26568	3.16	7.0E-05	AW847445.1	EST_HUMAN	repetitive element/contains element MSR1 repetitive element;
357	13688	26567	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
							RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
581	13773	26793	1.14	7.0E-05	L49076.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
581	13773	26794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1080	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15858	29008	6.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dictyostelium discoideum gene for TRFA, complete cds
4168	17318		0.85	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4482	17632	30614	1.88	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6041	18169	31144	0.88	7.0E-05	8845300	NT	Rat cytomegalovirus Measiticht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505582.1	EST_HUMAN	nt83g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:886086 3'
9753	22891	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04684 Fetal brain, Striatum (cat8363626) Homo sapiens cDNA clone HFBED80
11430	24481		5.87	7.0E-05	10633046	NT	Homo sapiens sarcoglycan, apelin (SGCE), mRNA
2083	16223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	15223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28882	1.66	6.0E-05	A1655241.1	EST_HUMAN	w654h05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2875	13880	28912	2.54	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32539	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6533	19697	33070	1.5	6.0E-05	N72829.1	EST_HUMAN	yw50g11.1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA897880.1	EST_HUMAN	q80a03.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504586 3'
8276	21358	34876	1.03	6.0E-05	BE094410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE094410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
8638	21718	35255	0.82	6.0E-05	AA160482.1	EST_HUMAN	208c08.s1 Scores_pregnant_uterus_Nbt-HPU Homo sapiens cDNA clone IMAGE:481728 3' similar to contains element MER28 repetitive element;
8843	21723	35280	2.62	6.0E-05	AW69829.1	EST_HUMAN	PM4-NN0050-310360-001-F10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q180401	SWISSPROT	COMPLEMENT DECAY ACCELERATING FACTOR PRECURSOR
9452	22568	36134	1.59	6.0E-05	P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (CABP)
9462	22568	36135	1.59	6.0E-05	P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (CABP)
8721	22788	36357	1.77	6.0E-05	T04149.1	EST_HUMAN	yec2c12.1 Stratiocane lung (8937210) Homo sapiens cDNA clone IMAGE:119082 5'
9922	22862	36550	0.69	6.0E-05	AW627985.1	EST_HUMAN	nt87a03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10987	24066	37701	2.42	6.0E-05	R75638.1	EST_HUMAN	y159d08.s1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:143635 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38495	2.7	6.0E-05	AA044015.1	EST_HUMAN	2k68f02.1 Soares_pregnant_uterus_NHMPU Homo sapiens cDNA clone IMAGE:487035 5'
12699	25999	31773	9.37	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-409 NT0038 Homo sapiens cDNA
1435	14598	27661	20.87	5.0E-05	AW392098.1	EST_HUMAN	QV4-ST0234-241198-040-h11 ST0234 Homo sapiens cDNA
1912	15065		1.07	5.0E-05	892389.1	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55385), mRNA
2924	16102	28116	0.84	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
4088	17243	30250	3.16	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5842	18836	31913	11.81	5.0E-05	X98886.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6115	19295	32630	3.58	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6297	19470	32825	0.97	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7486	20560		1.4	5.0E-05	AB037984.1	NT	Mus musculus gene for calretinin, exon 1
12498	25503		6.26	6.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868	13457		2.73	4.0E-05	P12821.1	NT	Human renin (REN) gene, 5' flanking region
4805	17742	30720	0.76	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4805	17742	30721	0.76	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4987	18126		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18266	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds
9723	22788		6.75	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10817	23651	37280	0.54	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)(ACID BETA-GALACTOSIDASE)
11007	24086	37723	4.14	4.0E-05	AW627948.1	EST_HUMAN	h38c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874980 3' similar to contains element MIR repetitive element:
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C082
12426	25302		1.47	4.0E-05	AW117580.1	EST_HUMAN	x833a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
13189	25773		1.16	4.0E-05	AA417758.1	EST_HUMAN	z001a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746262 3'
688	13881	25914	0.8	3.0E-05	A1248061.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element:
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16637		0.7	3.0E-05	A1288819.1	EST_HUMAN	q871g11.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:009632
4501	17641	30625	7.81	3.0E-05	BE169211.1	EST_HUMAN	008632 GLYCINE TYROSINE-RICH HAIR PROTEIN.:
4501	17641	30628	7.81	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4588	17725	30707	1.11	3.0E-05	AA388678.1	EST_HUMAN	EST79886 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4588	17725	30708	1.11	3.0E-05	AA368678.1	EST_HUMAN	EST789886 Placenta Homo sapiens cDNA similar to p53-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4889	13881	26014	0.7	3.0E-05	AJ248061.1	EST_HUMAN	qf94c10.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
5675	18693	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (MyLC2p), mRNA
5897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE733167.1	EST_HUMAN	601587451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8647	21628	35166	1.55	3.0E-05	AA284049.1	EST_HUMAN	z560D05.s1 Stragene echino brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9094	22173	35718	1.53	3.0E-05	AW770982.1	EST_HUMAN	H94408.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3008638 3'
9098	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407	36154	0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22586	36154	1.4	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22803	37403	3.62	3.0E-05	AJ789331.1	EST_HUMAN	wg36f09.x1 Soares NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10765	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25255		1.67	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12551	25374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12813	26106		1.29	3.0E-05	AW518689.1	EST_HUMAN	xs89d06.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2776811 3'
2400	15531	28658	1.49	2.0E-05	AJ286021.1	EST_HUMAN	qf98a11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2650	15773	28886	14.63	2.0E-05	M13782.1	NT	MER3 b2 MER3 repetitive element;
2777	15883		6.99	2.0E-05	AA160582.1	EST_HUMAN	Human adenocarcinoma deaminase (ADA) gene, complete cds
3207	16382	29393	1.29	2.0E-05	BE066036.1	EST_HUMAN	zq48a12.r1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:932734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3428	16597	29613	1.04	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-n08 BT0319 Homo sapiens cDNA
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3583	16748		0.87	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3909	17068		0.81	2.0E-05	AL039107.1	EST_HUMAN	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
5003	18132	31108	0.6	2.0E-05	AJ131016.1	NT	DKFZp568064.r1 568 (synonym: Ifhd2) Homo sapiens cDNA clone DKFZp568064 5'
5878	19083	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens SCL gene locus
6039	19222		0.87	2.0E-05	AF023308.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinase gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	18273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	18273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6286	19459	32811	0.79	2.0E-05	A1148272.1	EST_HUMAN	qp72a02.x1 Soares_placenta_8to9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'
6760	18916	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
7042	20095	33511	1.88	2.0E-05	Y08928.1	NT	nm08412.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238518 3'
7054	20107	33523	1	2.0E-05	A1482380.1	EST_HUMAN	P.falcipterus mRNA for AARP1 protein, partial
7062	20115		7.24	2.0E-05	A691025.1	EST_HUMAN	Q02711 PRO-POL-DUTPASE POLYPROTEIN;
7303	20385	33844	2	2.0E-05	AF224282.1	NT	w135h07.x1 Soares_Diethylstilbestrol_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7303	20385	33845	2	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
7624	20597		0.77	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
8089	21151	34671	1.58	2.0E-05	A381040.1	EST_HUMAN	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9467	22524	36087	0.59	2.0E-05	P49457	SWISSPROT	ig20f05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2106369 3'
9467	22524	36088	0.55	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10127	23105	36784	0.6	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10339	23374	36984	0.94	2.0E-05	BF055639.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	w175g08.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	w181a06.r1 Soares_placenta_8to9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:258570 5'
10881	20115		2.66	2.0E-05	A1691025.1	EST_HUMAN	w135h07.x1 Soares_Diethylstilbestrol_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11738	23924	37549	1.55	2.0E-05	BE176801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11681	24986	38688	5.74	2.0E-05	A1912713.1	EST_HUMAN	w12f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921 3'
12477	25921		3.7	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR-Q12832
12592	28104		8.13	2.0E-05	AW074604.1	EST_HUMAN	Q12832 GLYCOPHORIN HEP2;
							w189a03.x1 NCI_CGAP_Cor17 Homo sapiens cDNA clone IMAGE:2573832 3' similar to contains L1.13 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12650	25905		3.24	2.0E-05	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12625	25551	32014	2.01	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13208	25787		1.84	2.0E-05	AL200970.1	EST_HUMAN	q88g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765236 3'
2769	16071	28883	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	28905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17636	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	z469g04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4675	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	z449g11.x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5078	18207	31179	0.86	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
5084	18212	31185	0.84	1.0E-05	Z18943.1	NT	H. sapiens repeat region
6881	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20136	33553	4.24	1.0E-05	AA841848.1	EST_HUMAN	ns19g02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1
7232	20316	33769	5.19	1.0E-05	4505944	NT	L1 repetitive element;
7837	20892	34394	0.73	1.0E-05	BF222846.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21005		2.03	1.0E-05	P19474	SWISSPROT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8116	22195		2.39	1.0E-05	AL163272.2	NT	7p57d01.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3846945 3' similar to contains MER10 b3
9260	22337	35887	2.59	1.0E-05	AA452578.1	EST_HUMAN	MER10 repetitive element;
9487	22544	36107	12.29	1.0E-05	AA236110.1	EST_HUMAN	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9568	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
10043	23081	36882	0.79	1.0E-05	AW510602.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
10043	23081	36883	0.79	1.0E-05	AW510602.1	EST_HUMAN	z36h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:788519 3' similar to
10120	23158	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	gbxL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10120	23158	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	z505e11.t1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu
10387	23422		2.04	1.0E-05	AW465956.1	EST_HUMAN	repetitive element; contains element TAR1 repetitive element;
							AV732190 HTF Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.t1 OFR repetitive element;
							hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.t1 OFR repetitive element;
							UIH-B12-egk-a-08-0-UJ.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							UIH-B12-egk-a-08-0-UJ.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							hd07c10.x1 NCI CGAP_K1412 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1
							repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11159	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	28036	31683	1.4	1.0E-05	AL163303.2	NT	Human sapiens chromosome 21 segment HS21G103
2737	15854	28868	5.83	9.0E-06	AI583811.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21G103
3165	18340	28348	6.11	9.0E-06	AL218083.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21G103
3698	16859		2.56	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6025	19208	32528	2.48	9.0E-06	L23416.1	NT	Human sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-06	BE065042.1	EST_HUMAN	RC1-9T0313-110500-017-a07 BT0313 Homo sapiens cDNA
7698	20668	34144	2.82	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7963	21003	34515	12.35	9.0E-06	AK034370.1	EST_HUMAN	cc20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1658912 3' similar to contains Alu repetitive element
8669	21739	35280	1.17	9.0E-06	AL160208.2	NT	Homo sapiens chromosome 21 segment HS21G009
8183	22261	35803	3.3	9.0E-06	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8183	22261	35804	3.3	9.0E-06	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37883	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2598	16085	28839	2.01	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33278	2.75	8.0E-06	AA284847.1	EST_HUMAN	z122d06.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MERB.11 MERB repetitive element
10751	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCDILIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCDILIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	ab30H10.s1 Striatogene lung (8337210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20 H1 MER20 repetitive element
1470	14624	27708	3.12	7.0E-06	7682177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2836	16113		10.59	7.0E-06	AI388252.1	EST_HUMAN	qwt6g09.x1 NC1_CGAP_U33 Homo sapiens cDNA clone IMAGE:1891286 3' similar to contains Alu repetitive element
3654	16817		0.85	7.0E-06	AA388542.1	EST_HUMAN	EST189205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-08	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5825	19112	32424	0.93	7.0E-08	N98845.1	EST_HUMAN	y65507.f1 Soares_multiple_sclerosis_2Nb-IMPSP Homo sapiens cDNA clone IMAGE:278412 5'
8889	22088	35508	0.83	7.0E-08	11420708	NT	Homo sapiens DNA segment, numerous copies, expressed probes (Q91 gene) (DXF88S1E), mRNA
10104	23142		0.52	7.0E-08	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31547	1.88	7.0E-08	BF215872.1	EST_HUMAN	601881522F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4083072 5'
2884	16100	29177	1.17	6.0E-08	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3784	16945	29852	1.02	6.0E-08	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4878	16183	29208	2.13	6.0E-08	Q01458	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4883	18013	30597	2.19	6.0E-08	A1040039.1	EST_HUMAN	cod8e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1665738 3' similar to contains MER8.12 MER8 repetitive element:
5465	18885	31844	2.29	6.0E-08	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5525	18722	31739	1.16	6.0E-08	C02040	SWISSPROT	PROTEIN XE7
10080	23098		1.96	6.0E-08	AW801912.1	EST_HUMAN	IL5-JM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13142	25742	31948	2.39	6.0E-08	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6186	19382	32710	3.74	5.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
6467	19834	32995	1.94	5.0E-08	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8804 Met protein (M8804 Met) gene, complete cds
7382	20460	33923	1.18	5.0E-08	AB007546.1	NT	Homo sapiens gene for LEO12, complete cds
8654	21734	35274	0.58	5.0E-08	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-08	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
10307	23942	36947	6.96	5.0E-08	AA313820.1	EST_HUMAN	EST185488 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
10731	23764	37372	0.61	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25686	31957	5.49	5.0E-08	A105045.1	EST_HUMAN	HA08777 Human fetal liver cDNA library Homo sapiens cDNA
684	13850	26877	5.47	4.0E-08	R16267.1	EST_HUMAN	ya4603.f1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element:contains L1 repetitive element:
889	14045	27110	4.73	4.0E-08	AW103354.1	EST_HUMAN	x063g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2588574 3' similar to contains Alu repetitive element:contains element MER21 repetitive element:
1365	14519	27698	3.18	4.0E-08	A1334928.1	EST_HUMAN	IB33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1365	14519	27594	3.18	4.0E-08	A1334928.1	EST_HUMAN	IB33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1503	14656	27738	1.45	4.0E-08	BF368612.1	EST_HUMAN	QV2-NT0046-200600-250-H07 NT0046 Homo sapiens cDNA
2339	15470	28805	1.96	4.0E-08	AW015401.1	EST_HUMAN	U1-H-B10-est-f-05-O-U1.g1 NCI_CGAP_Sub01 Homo sapiens cDNA clone IMAGE:2710425 3'
3131	16307	29321	0.89	4.0E-08	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-08	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4020	18053	31041	1.88	4.0E-08	AB869339.1	EST_HUMAN	w94c10.x1 NCL CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
8696	21776	36308	0.68	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
8000	22079	35620	4.49	4.0E-08	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8909	22949	36535	1.28	4.0E-08	AJ272665.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11735	23921	37546	3.99	4.0E-08	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
13149	26152		1.33	4.0E-06	AW260734.1	EST_HUMAN	xs53e01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	z534b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2232	15366	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	z534b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2340	15471		1.48	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2698	16184	28180	0.84	3.0E-08	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.53 LTR1 repetitive element;
3339	16512		2.67	3.0E-06	AI857778.1	EST_HUMAN	w122a05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
3883	17042	30040	1.47	3.0E-08	BE047084.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3883	17042	30041	1.47	3.0E-08	BE047084.1	EST_HUMAN	hg64412.x1 NCL CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4597	17734	30714	0.8	3.0E-06	TS0266.1	EST_HUMAN	hg64412.x1 NCL CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4684	17818	30807	5.62	3.0E-08	X54916.1	NT	y578b10.r1 Stratiogene ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
6288	19482	32614	0.82	3.0E-08	AU159412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunlin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
7377	20458		2.14	3.0E-08	P08548	SWISSPROT	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001802 3'
8274	21366	34874	0.81	3.0E-08	BE562384.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8883	21982	35496	0.76	3.0E-08	P07743	SWISSPROT	60136213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680314 5'
12856	25435		12.07	3.0E-08	AW385282.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
207	19430		2.22	2.0E-08	P54368	SWISSPROT	RCO-LT0001-261198-011-A03 LT0001 Homo sapiens cDNA
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
2451	15579	28707	2.58	2.0E-08	A672138.1	EST_HUMAN	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2537	15682	28785	1.69	2.0E-06	P04829	SWISSPROT	w804a03.x1 NCL CGAP_JGd11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1
2632	15755	28870	1.81	2.0E-06	P06719	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3607	15771	29786	0.9	2.0E-06	AV657555.1	EST_HUMAN	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
							AV657555 GLC Homo sapiens cDNA clone GLC-FD806 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3868	17018	30017	1.54	2.0E-08	AA173518.1	EST_HUMAN	zp0205.r1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:585232 5'
3868	17027	30026	0.89	2.0E-08	AW450215.1	EST_HUMAN	U1H-B13-alky-g-05-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3876	17035	30033	1.7	2.0E-08	AB030898.1	NT	Mus musculus gene for odorant receptor A10, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6246	19420	32766	0.82	2.0E-08	AI630448.1	EST_HUMAN	ts51f05.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2080241 3' similar to TR:Q13537
6571	19733	33112	5.64	2.0E-06	AB18424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7635	20704	34183	0.83	2.0E-08	AA688423.1	EST_HUMAN	W90604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184		1.02	2.0E-06	AW1869223.1	EST_HUMAN	nv58c06.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1234060 3' similar to contains L1.13 L1
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	repetitive element;
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	NR3-SN0067-120400-002-f02 SN0067 Homo sapiens cDNA
9046	22128	35972	1.59	2.0E-08	H62051.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9417	22491	36056	0.9	2.0E-06	AF003528.1	NT	zh27c11.s1 Soares_pituitary_gland_N31-IPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9417	22491	36057	0.9	2.0E-06	AF003528.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9436	22610		0.46	2.0E-06	AI473450.1	EST_HUMAN	y487c04.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gbX74928
9802	22942	36627	0.86	2.0E-06	N30576.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10123	23161		0.7	2.0E-06	AV748969.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
12548	26135	31549	1.34	2.0E-06	P23249	SWISSPROT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	t18g110.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
34	13272	26276	1.16	1.0E-06	OT6082	SWISSPROT	yw66a03.s1 Soares_placenta_8to9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
674	13860	26891	1.8	1.0E-06	AF084364.1	NT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
1482	14635	27719	1.8	1.0E-06	PO9125	SWISSPROT	PROTEIN MOV-10
1553	14708	27768	1	1.0E-06	AL163278.2	NT	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	repetitive element;
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	Mus musculus DNMM5E protein (D6Mm59) mRNA, complete cds
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	z06a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	contains Alu repetitive element;
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	z06a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1815	14768		0.99	1.0E-06	P27825	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2060	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4489	17929	30610	15.97	1.0E-06	U07661.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8504 Met protein (M8504 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-06	N65948.1	EST_HUMAN	zz27a08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:263750 3'
5405	18607	31679	5.14	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-06	C00013	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5615	18103		0.72	1.0E-06	BC063527.1	EST_HUMAN	CMB-BT0281-031198-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7923	26223		0.73	1.0E-06	BE185380.1	EST_HUMAN	IL6-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8190	21272		0.98	1.0E-06	AA912623.1	EST_HUMAN	cd28c08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8468	21549	35079	1.12	1.0E-06	AB347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8685	21795	35297	1.31	1.0E-06	AL287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
8904	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element
9578	22721	36291	0.61	1.0E-06	Q38575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-06	U82698.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-06	U82698.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22969	36558	5.22	1.0E-06	AA132811.1	EST_HUMAN	zo17e08.l1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	zo04d11.s1 Soares total fetus NB2HF8_9w Homo sapiens cDNA clone IMAGE:765493 3' similar to
10705	23738		2.19	1.0E-06	AL163203.2	NT	gtd28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11949	24935		3.1	1.0E-06	AW890941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12598	25398	32041	8.24	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
371	13680	26613	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8902	21683		0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
4893	18023	31008	4.23	8.0E-07	AL288598.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
							ql82g07.x1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1878676 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession - No.	Top Hit Database Source	Top Hit Descriptor
4893	18023	31009	4.23	8.0E-07	A288598.1	EST_HUMAN	q182p07.x1 Soares_NhiHMP_u_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
6007	19182		8.17	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8191	21273		8.44	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glycucuronosyltransferase gene, complete cds
11021	24007		5.84	8.0E-07	T07770.1	EST_HUMAN	EST050600 Fetal brain, Striatogene (cat#930206) Homo sapiens cDNA clone HFBEN69
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31906	0.86	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1962	15105	28205	3.47	6.0E-07	AW85558.1	EST_HUMAN	CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2561	15888	28812		6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heilacase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4P33 INTERGENIC REGION
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	7g9407.x1 NCL_CGAP_Col16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 075920 4FSL;
12115	25085	39800	1.45	6.0E-07	BE063508.1	EST_HUMAN	CM0-BT0281-031189-087-e03 BT0281 Homo sapiens cDNA
12444	26087		1.72	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-H12 NN1029 Homo sapiens cDNA
13229	25992		1.32	6.0E-07	BE222390.1	EST_HUMAN	hul11h05.x1 NCL_CGAP_Lu024 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1 repetitive element;
336	13549		1.04	5.0E-07	AJ831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2985547 3'
1082	14248		2.89	6.0E-07	AA380630.1	EST_HUMAN	EST83615 Supt cells Homo sapiens cDNA 5' end
3096	16272		0.79	5.0E-07	AJ831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2985547 3'
4769	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exon 4 through 14 and complete cds
6247	19421	32767	1.33	5.0E-07	U69067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7210	20075	33487	1.71	5.0E-07	AJ389881.1	EST_HUMAN	tg06b005.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7210	20075	33488	1.71	5.0E-07	AJ389881.1	EST_HUMAN	tg06b005.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7503	20578	34050	16.93	5.0E-07	AW070883.1	EST_HUMAN	xs31a02.x1 NCL_CGAP_B118 Homo sapiens cDNA clone IMAGE:2588362 3' similar to gb:X16341
8470	21651	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8687	21767		0.88	5.0E-07	P09593	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
							S-ANTIGEN PROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23612	37217	5.47	5.0E-07	A088587.1	EST_HUMAN	CH-ET178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.68	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24868		2.08	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12258	25968		1.2	5.0E-07	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
12918	26966		3.08	5.0E-07	AW862537.1	EST_HUMAN	QV6-CT03883-210400-204-512 CT03883 Homo sapiens cDNA
4108	17260	30261	1.66	4.0E-07	AW009602.1	EST_HUMAN	WS84105.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:2604687 3'
7328	20410		0.8	4.0E-07	AJ272265.1	NT	Homo sapiens SPPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20495	33983	0.97	4.0E-07	Q922V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20495	33984	0.97	4.0E-07	Q922V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8261	22328	35875	4.9	4.0E-07	AW418134.1	EST_HUMAN	3x49g11.x1 NCI_CGAP_LUG4.1 Homo sapiens cDNA clone IMAGE:2885548 3'
10332	23367	36978	0.63	4.0E-07	BE001975.1	EST_HUMAN	001076748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956851 5'
10332	23367	36977	0.53	4.0E-07	BE001976.1	EST_HUMAN	001076748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956851 5'
10531	23566	37174	0.58	4.0E-07	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	AJ765528.1	EST_HUMAN	W81B08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
11179	24248	37882	3.88	4.0E-07	AJ765528.1	EST_HUMAN	W81B08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
11495	24553		1.68	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
11818	24906		1.32	4.0E-07	BE867557.1	EST_HUMAN	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932924 5'
13207	25798		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26886	5.39	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
698	13786	26806	3.59	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1405	14559	27633	1.43	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1655	14808		3.62	3.0E-07	M94857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2104	15243		2.32	3.0E-07	AA526763.1	EST_HUMAN	ni56b108.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:380825 similar to contains Alu repetitive element; contains L1.9 L1 repetitive element
2361	15492	28621	1.14	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2540	15665	28789	4.98	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2540	15665	28789	4.98	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3058	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	y550f12.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111636 5'
3228	16402	28414	1.78	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4802	17837		0.64	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVONACROGLOBULIN)
4849	17882	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 5'
4895	18015	30989	0.7	3.0E-07	AJ767236.1	EST_HUMAN	WS86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347887 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6175	18267	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6175	18267	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6783	18975	32281	12.38	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6895	19276	32605	0.7	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	18996		5.09	3.0E-07	AA815175.1	EST_HUMAN	cc04c10.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1389890 3'
7678	20743	34224	3.63	3.0E-07	AW787168.1	EST_HUMAN	QV1-JM0038-200300-116-g02 UM0038 Homo sapiens cDNA
7841	20893		1.3	3.0E-07	A1591065.1	EST_HUMAN	tw28f11.s1 NCI CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1
8330	22406	35059	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
8330	22406	35060	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13184	25777		4.28	3.0E-07	AJ132362.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
28	13267	26270	7.32	2.0E-07	AF262888.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26413	6.06	2.0E-07	L77569.1	NT	Homo sapiens Digeorge syndrome critical region, telomeric end
158	13383	26414	6.06	2.0E-07	L77569.1	NT	Homo sapiens Digeorge syndrome critical region, telomeric end
186	13403	26437	35.88	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vesicular) actin gene, complete cds
767	13948	26695	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
767	13948	26696	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
966	14139	27200	2.32	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stragene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
967	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element
1189	14351	27400	1.55	2.0E-07	O26768	SWISSPROT	I16 AUTOANTIGEN
1630	14782	27688	2.08	2.0E-07	Q09701	SWISSPROT	HYPOPHOSPHATE 72.5 KD PROTEIN C27.10 IN CHROMOSOME 1
3708	18869		0.63	2.0E-07	BF191397.1	EST_HUMAN	601818616F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3779	18940	28946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6480	18680	31638	1.52	2.0E-07	AW680068.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	26829	33229	0.73	2.0E-07	AW448988.1	EST_HUMAN	UHH-B19-ale-b-01-Q-U1.s1 NCI_CGAP Sub6 Homo sapiens cDNA clone IMAGE:2794008 3'
6802	18957	33357	3.39	2.0E-07	AL208716.1	EST_HUMAN	qp56d05.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8694	21744		3.37	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAE302 5'
8693	21972	35508	1.11	2.0E-07	AA035188.1	EST_HUMAN	zk27g08.a1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
8693	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW602507.1	EST_HUMAN	CHM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10708	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10708	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBP2)
12138	26656		2.96	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12228	25997		2.38	2.0E-07	AF732462.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBP2)
1126	14281		0.76	1.0E-07	AL163282.2	NT	PM4-HT0339-260100-008-H07 HT0339 Homo sapiens cDNA
2888	14704	27784	2.08	1.0E-07	P09258	SWISSPROT	zn85h11.x5 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR.b2 THR repetitive element
3838	14291		1.24	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4408	17660	30534	2.91	1.0E-07	AV718682.1	EST_HUMAN	GLYCOPROTEIN GPV
4408	17650	30535	2.91	1.0E-07	AV718682.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
							Homo sapiens chromosome 21 segment HS21C082
6832	19791	33180	0.8	1.0E-07	UB2871.2	NT	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
7006	20142	33560	4.69	1.0E-07	BE047874.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
7006	20142	33561	4.69	1.0E-07	BE047874.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calitractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7682	20728	34205	7.6	1.0E-07	N55081.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281339 5'
7826	20881	34382	0.69	1.0E-07	BF375909.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281339 5'
7826	20881	34383	0.69	1.0E-07	BF375909.1	EST_HUMAN	y43c07.a1 Soares_fetal_liver_spleen_TNPLS Homo sapiens cDNA clone IMAGE:245484 3'
7854	20909	34413	1.24	1.0E-07	AL163281.2	NT	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8410	21491	35021	2.76	1.0E-07	P97435	SWISSPROT	Homo sapiens chromosome 21 segment HS21C081
9155	22233	35778	2.7	1.0E-07	AA683576.1	EST_HUMAN	ENTEROPEPTIDASE (ENTEROKINASE)
							ENTEROPEPTIDASE (ENTEROKINASE)
							ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS B) (ADAMTS-8) (ADAM-TS8) (METH-2)
9470	22527	36080	1.05	1.0E-07	P57110	SWISSPROT	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22898	36436	0.6	1.0E-07	BE327843.1	EST_HUMAN	h128h06.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36776	2.35	1.0E-07	BF974524.1	EST_HUMAN	MER18 repetitive element;
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
10682	23716		1.22	1.0E-07	AL163282.2	NT	EST185054 Bratin IV Homo sapiens cDNA
12085	25065	36771	2.35	1.0E-07	AB341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12508	25339	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	q689603.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2009682 3'
12568	25438		1.45	1.0E-07	XB4467.1	NT	tr53c11.x1 NCI_CGAP_K0d11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-O65722 O65722
12852	25568		2.1	1.0E-07	XS1755.1	NT	DJ1163J1.1;
7433	20510	33982	0.75	9.0E-08	AI63362.1	EST_HUMAN	H. sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	tr551006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080185 3'
11965	24950	38656	2.38	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone c0481F808 5'
12458	25320		2.51	9.0E-08	AJ251973.1	NT	tr30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element;
1075	14241		1.01	8.0E-08	BE795489.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3634	16798		1.57	8.0E-08	BE795489.1	EST_HUMAN	Homo sapiens partial steelfr-1 gene
8937	22016	36557	5.35	8.0E-08	AI752387.1	EST_HUMAN	tr16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22016	35558	5.35	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9827	22867	36449	3.03	8.0E-08	AW970893.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	cnr15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnr15c02 random
11523	24579		1.73	8.0E-08	AF23417.1	NT	cnr15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnr15c02 random
82	13317	26345	3.91	7.0E-08	Q02257	SWISSPROT	EST1362778 IMAGE resequences, MAGK Homo sapiens cDNA
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3656	16829	29839	0.85	7.0E-08	P15305	SWISSPROT	Homo sapiens mitochondrial epoxide hydrolase (EPHX1) gene, complete cds
3666	16829	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
6332	18445	31413	0.62	7.0E-08	T85891.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI635743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11970	24955	38658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12978	16829	28839	1.84	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16829	28840	1.84	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15504	28663	1.77	6.0E-08	BE144398.1	EST_HUMAN	MRO-H70168-191189-004-g08 HT0168 Homo sapiens cDNA
3129	16305	28319	0.68	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4363	17806	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9629	22504		0.55	6.0E-08	AA827075.1	EST_HUMAN	cb56c05.s1 NCI_CGAP_GCBI Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24698	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11823	24812		1.43	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2309	16441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
12185	25144		4.55	6.0E-08	P08681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25271	32077	1.77	5.0E-08	AW851878.1	EST_HUMAN	QV6-CT0225-131088-034-a12 CT0225 Homo sapiens cDNA
1789	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
1789	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
2560	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_J1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp434J0426 5'
3132	16308		1.01	4.0E-08	AI078417.1	EST_HUMAN	ca05602.x1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6535	18698	33071	1.07	4.0E-08	P62624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8668	22077	38617	0.9	4.0E-08	O15983	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
9340	22416	38689	1.13	4.0E-08	L42871.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
8846	22865		1.56	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10336	23571		0.85	4.0E-08	AI016942.1	EST_HUMAN	cd78d12.s1 Soares fetal testis_Nb2-HF8_Bw Homo sapiens cDNA clone IMAGE:1622803 3'
10597	23832	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	ar22d10.x1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA398627.1	EST_HUMAN	2766b08.t1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:78247 5' similar to TR-G505579 G505579 NA/Ca-K-EXCHANGER ;

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11328	24391	38038	5.16	4.0E-08	AA383627.1	EST_HUMAN	z47608.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:Q505579
11349	24411	38084	11.88	4.0E-08	BF682493.1	EST_HUMAN	G605579 NAUCA_K-EXCHANGER. ;
11349	24411	38065	11.88	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333300 5'
12160	28108		1.93	4.0E-08	W76158.1	EST_HUMAN	602248024F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333300 5'
12804	26698		2.01	4.0E-08	AI343353.1	EST_HUMAN	z485g03.1 Scores_fetal_heart_NbH110W Homo sapiens cDNA clone IMAGE:345558 5' similar to contains L1.H1 L1 repetitive element ;
5728	18921	32215	2.27	3.0E-08	BE018348.1	EST_HUMAN	tf585a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
7115	18541	31498	6.01	3.0E-08	AI782737.1	EST_HUMAN	MER18 MER18 repetitive element ;
7711	20776	34262	1.43	3.0E-08	AL163246.2	NT	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z168 Q9Z168 SYNTAXIN 17. ;
7928	20978		3.32	3.0E-08	AI436352.1	EST_HUMAN	qs76111.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
10102	23140		0.83	3.0E-08	AF050596.1	NT	Homo sapiens chromosome 21 segment HS21C046
11278	24343	37983	1.64	3.0E-08	AI218001.1	EST_HUMAN	th63109.x1 Scores_NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
11957	24942	38848	1.32	3.0E-08	AF111167.2	NT	Homo sapiens MHC class 1 region
12196	25123		33.85	3.0E-08	R18420.1	EST_HUMAN	qh21a04.x1 Scores_NFL_T_Q8C_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
211	13434		4.16	2.0E-08	AW302896.1	EST_HUMAN	Homo sapiens Jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene repetitive element ;
236	19458		5.76	2.0E-08	AA425598.1	EST_HUMAN	yg02004.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:309448 5' similar to contains Alu repetitive element ;
509	13703	28732	4.46	2.0E-08	AF198349.1	NT	z48507.1 Scores_total_fetus_Nb21F8_gW Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element ;
677	13863	26893	9.7	2.0E-08	AW888438.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
677	13863	26894	9.7	2.0E-08	AW888438.1	EST_HUMAN	MFO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	14186		7.75	2.0E-08	BE280477.1	EST_HUMAN	MFO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	601166321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138868 5'
1774	14823	28017	0.98	2.0E-08	AW841880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
1780	14829		2.08	2.0E-08	BE734871.1	EST_HUMAN	LB-CN0024-030300-028-C01 CN0024 Homo sapiens cDNA
1902	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5'
2608	15732		1.86	2.0E-08	K00216.1	NT	xp43911.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
3279	18453	29474	5.61	2.0E-08	O42280	SWISSPROT	Sheep His-RNA-GUG
							WNT-14 PROTEIN PRECURSOR

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3279	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3662	17120		1.63	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4169	17339	30332	0.62	2.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17684		1.46	2.0E-08	AA4590.40.1	EST_HUMAN	aa26c07.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5072	18200		3.5	2.0E-08	AW572681.1	EST_HUMAN	he17f08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1377189 3'
5955	19141	32457	1	2.0E-08	AW088824.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
6163	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8301	21383	34904	1.5	2.0E-08	AA460121.1	EST_HUMAN	POL POLYPOLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9288	22362		0.89	2.0E-08	AU136878.1	EST_HUMAN	cd02g08.t1 Strabagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:830674 3'
10738	23771	37381	0.89	2.0E-08	N78097.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10738	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	yw7202.j1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12476	25329		1.77	2.0E-08	AL163284.2	NT	yw7202.j1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
13065	26159		1.8	2.0E-08	11431678	NT	Homo sapiens chromosome 21 segment HS21O84
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	Homo sapiens hypodermal protein FLJ11342 (FLJ11342), mRNA
1672	14824	27607	1.33	1.0E-08	P13002	SWISSPROT	POL POLYPOLYPROTEIN[CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1672	14824	27608	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1)(ELEMENT BINDING ACTIVITY)
1816	14895	28058	1.66	1.0E-08	AF125348.1	NT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1)(ELEMENT BINDING ACTIVITY)
2110	15248		2.97	1.0E-08	BE141859.1	EST_HUMAN	(TRANSCRIPTION FACTOR NTF-1)
3261	16435	29453	0.95	1.0E-08	BE246844.1	EST_HUMAN	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1)(ELEMENT BINDING ACTIVITY)
3261	16435	29454	0.95	1.0E-08	BE246844.1	EST_HUMAN	(TRANSCRIPTION FACTOR NTF-1)
6716	18009	32204	4.51	1.0E-08	AJ010770.1	NT	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
7946	20986	34507	0.94	1.0E-08	P19474	SWISSPROT	PM2-HT0130-150959-001-f12 HT0130 Homo sapiens cDNA
8224	21308	34826	0.62	1.0E-08	AL163302.2	NT	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
							TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
							Homo sapiens hyperion gene, exons 1-50
							62 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
							Homo sapiens chromosome 21 segment HS21C102

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8320	21402	34927	0.54	1.0E-08	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	AI016304.1	EST_HUMAN	635a05.s1 Soares_hes3_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22479		0.56	1.0E-08	P08563	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA
10171	23208	36801	0.94	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10778	23811	37434	0.87	1.0E-08	P08063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11593	24648	38332	3.55	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12881	25391		3.06	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
13137	25925		1.26	1.0E-08	BF375398.1	EST_HUMAN	Human lambda5-immunoglobulin constant region complex (germline)
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10267	23302		0.63	9.0E-09	T97850.1	EST_HUMAN	Homo sapiens fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7414	20482	33960	8.1	8.0E-09	AI183500.1	EST_HUMAN	ye58a12.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1732164 3' similar to qd42a07.x1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element
8189	21271	34798	2.54	8.0E-09	AW1900159.1	EST_HUMAN	CM0-NN1004-100300-273-908 NN1004 Homo sapiens cDNA
8189	22267		2.53	8.0E-09	AA938892.1	EST_HUMAN	op74008.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582576 3'
3695	16896		1.96	7.0E-09	D88842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4115	17269		0.96	7.0E-09	U50671.1	NT	Human familial Alzheimer's disease (S1M2) gene, complete cds
8088	21168		0.58	7.0E-09	BF108766.1	EST_HUMAN	7445a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.b2 MER29 repetitive element
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr60c05.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:681892 5' similar to contains L1.12 L1 repetitive element
9460	22517	36090	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10396	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3331834 5'
10554	23580		0.78	7.0E-09	AA058626.1	EST_HUMAN	zf58a07.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element
10910	23983		2.01	7.0E-09	T97850.1	EST_HUMAN	ye58a12.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2221	15355		0.95	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-H05 HT0527 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6498	18886	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	x085f083.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35396	1.11	6.0E-09	BE161663.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 9 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23618		3.4	6.0E-09	AF200929.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10669	24049	37682	1.66	6.0E-09	BF108755.1	EST_HUMAN	7456f10.x1 Soares_NSIF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12089	25069	38776	1.37	6.0E-09	CO1803.1	EST_HUMAN	HUMG0003762 Human adult (K.Ohara) Homo sapiens cDNA
1447	14800	27677	3.47	5.0E-09	BE148284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1600	16043	28154	7.4	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6640	19703	33076	2.22	6.0E-09	AA359454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV231A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV7S2A1N4T, TCRBV6S1P, TCRBV7S3A2T, TCRBV1SS2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV1SS913S>
6988	18507	31523	0.66	5.0E-09	U66059.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8785	21894	35407	0.83	6.0E-09	P37071	SWISSPROT	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
10300	23395	36940	3.25	5.0E-09	AW769667.1	EST_HUMAN	z60e09.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:765880 3'
11944	24930	36832	1.87	5.0E-09	AA460142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
634	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens hypophyseal protein (AF038169), mRNA
1497	14850	27782	1.66	4.0E-09	9558718	NT	EST68385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2500	15827	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	z404c08.f1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	y411a07.x1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:86804 3'
8719	21789	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	vm04f10.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2449827 3'
11330	24393	38041	9.51	4.0E-09	A1896401.1	EST_HUMAN	z344f12.f1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:U07807 DYNAMIN-1 (HUMAN);
11379	24440		1.44	4.0E-09	AA186142.1	EST_HUMAN	h009e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2427	15555	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2816	15742	28858	1.05	3.0E-09	BE222239.1	EST_HUMAN	h009e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2716	16834	28944	0.69	3.0E-09	P23249	SWISSPROT	MER18 repetitive element;
							PROTEIN MOV-10
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	h009e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							MER18 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3484	18331		0.7	3.0E-09	AA42272.1	EST_HUMAN	z64604.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:767422 5'
4212	17391		0.82	3.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4548	17694	30668	3.47	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4634	17770	30751	1.19	3.0E-09	Q973R5	SWISSPROT	238.1 KDA PROTEIN C21ORF5 (KIAA0893)
8084	21168	34682	1.1	3.0E-09	BE465780.1	EST_HUMAN	h080402.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194080 3' similar to TR-O55091
10453	23498	37096	1.87	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN. ;
10782	23825	37448	0.49	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37976	3.15	3.0E-09	BF109943.1	EST_HUMAN	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37979	3.15	3.0E-09	BF109943.1	EST_HUMAN	7172b08.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.88	2.0E-09	X16674.1	NT	7172b08.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1681	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	H.sapiens chromosome 21 segment HS21C084
2403	15534	28681	2.24	2.0E-09	Q973R5	SWISSPROT	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 6'
4048	17204	30214	3.01	2.0E-09	O60241	SWISSPROT	238.1 KDA PROTEIN C21ORF5 (KIAA0893)
4119	17273	30272	0.9	2.0E-09	AL263479.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5264	18383	31348	0.82	2.0E-09	M23161.1	NT	q07d09.x1 Scores_NHIMP_u_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5837	19027	32333	0.87	2.0E-09	A004082.1	EST_HUMAN	Human transposon-like element mRNA
6278	19452		0.75	2.0E-09	AL163249.2	NT	cd47b09.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST166142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7682	20757	34242	0.86	2.0E-09	W26834.1	EST_HUMAN	z653106.r1 Scores_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:766187 5' similar to contains
7971	21021	34534	0.59	2.0E-09	AL243732.1	EST_HUMAN	Alu repetitive element;
8909	21988	35528	1.2	2.0E-09	AJ271736.1	NT	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
10824	23957	37480	0.85	2.0E-09	AV888942.1	EST_HUMAN	q188g10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1864114 3'
12745	14013		20.08	2.0E-09	X16674.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12830	26188		1.86	2.0E-09	AA226070.1	EST_HUMAN	AV688842 GKX Homo sapiens cDNA clone GKACAC11 5'
1019	14190		1.19	1.0E-09	W78152.1	EST_HUMAN	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1133	14298	27353	1.43	1.0E-09	5031624	NT	nc11c02.r1 NC1_CGAP_Py1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive
1133	14298	27354	1.43	1.0E-09	5031624	NT	element;
							z678403.s1 Scores_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
							gb102892 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
							Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
							Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	15698		1.15	1.0E-09	AB56086.1	EST_HUMAN	q64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2010812 3' similar to contains MIER12.12 MIER12 repetitive element;
2584	16131	29149	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
2592	16168	29184	6.17	1.0E-09	M28698.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2592	16168	29185	6.17	1.0E-09	M28698.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16278	29293	0.99	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds 601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4920	18050		6.15	1.0E-09	AA719287.1	EST_HUMAN	zh35k03.x1 Soares_pineal_gland_NSHPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5341	18454		0.8	1.0E-09	AA921958.1	EST_HUMAN	cm44g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5620	18814	31882	0.95	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
5652	19138	32454	1.28	1.0E-09	U07090.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19446	32784	3.34	1.0E-09	P26864	SWISSPROT	CIRCUMSPOROITE PROTEIN PRECURSOR (CS)
8594	21665	35206	0.92	1.0E-09	A168474.1	EST_HUMAN	w439005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.H1 MER25 repetitive element;
10620	23555		2.72	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
12642	26120	31698	1.71	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12767	25510		1.42	1.0E-09	T57366.1	EST_HUMAN	y651g12.s1 Streptococcus faecalis spleen (#637205) Homo sapiens cDNA clone IMAGE:74758 3'
13132	26020		1.66	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14484	27564	1.62	9.0E-10	AW867740.1	EST_HUMAN	MRO-SIN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2695	16074	26092	3.74	9.0E-10	A1870071.1	EST_HUMAN	w678h03.x1 Soares_Dieckgrafe_coton_NHCD Homo sapiens cDNA clone IMAGE:2347283 3' similar to SW:RL29_HUMAN P47014 60S RIBOSOMAL PROTEIN L29 ; contains element P71R5 repetitive element ;
6973	20201	33627	4.98	9.0E-10	A1452882.1	EST_HUMAN	q48b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144637 3' similar to TR:O00372 O00372 PUTATIVE P160. ;
151	13376	28408	9.26	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	28607	0.86	8.0E-10	BE080748.1	EST_HUMAN	QV1-B170631-150200-071-401 BT0631 Homo sapiens cDNA
4318	17461	30446	5.45	8.0E-10	AA376832.1	EST_HUMAN	EST188564 Small intestine 1 Homo sapiens cDNA 5' end
10170	23207		2.51	8.0E-10	U36306.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
719	13901	26942	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1681	14804	27680	2.98	7.0E-10	Q19342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2626	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3167	16332	26941	2.25	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6314	19488	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7574	20846	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-208-D12 HT0619 Homo sapiens cDNA
7834	20889		1.85	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
836	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2742	16859	28971	1.63	6.0E-10	A424405.1	EST_HUMAN	LOC2407.X1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2085021 3'
4615	17752	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4881	17894		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031059-012-g12 CT0254 Homo sapiens cDNA
8983	22082	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8983	22082	35603	0.96	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
8984	22874	36458	0.48	6.0E-10	P88073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
12223	25172		1.95	6.0E-10	AW971823.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
780	13960		5.29	5.0E-10	AL046804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3564	16729	26745	1.14	5.0E-10	Q01033	SWISSPROT	EST384012 MAGe resequences, MAGL Homo sapiens cDNA
5105	18233	31202	1.4	6.0E-10	AF181887.1	NT	DKFZp434N219.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
7475	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	Maceoa tonkeana isolate 5890000000 NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
114	13345		1.09	4.0E-10	AJ221083.1	EST_HUMAN	cg09009.x1 Soares_placenta_806weeks_ZNtHP80c6W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR.b2 LTR8 repetitive element;
2062	15183	28306	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg55g03.x1 NCL CGAP_G03 Homo sapiens cDNA clone IMAGE:2048944 3' similar to contains Alu repetitive element;
2840	15763	28877	6.79	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7327	20406	33871	17.76	4.0E-10	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	UIH-B12-eH-a-07-QJL51 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10682	23696	37305	1.12	4.0E-10	AJ267342.1	EST_HUMAN	eq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-08 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-08 HT0521 Homo sapiens cDNA
838	14112	27173	2.24	3.0E-10	N38113.1	EST_HUMAN	y93206.s1 Soares melanocyte 2N1H1M Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element:
1382	14537		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4657	17763	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17763	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
6360	18463	31428	0.89	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5571	18767	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	Human XRCO1 DNA repair gene, genomic
6332	19503	32861	2.06	3.0E-10	P20360	SWISSPROT	Y21108.s1 Soares multiple sclerosis 2N1H1MSP Homo sapiens cDNA clone IMAGE:282782 3'
6481	18048	33010	3.82	3.0E-10	BE302870.1	EST_HUMAN	RHOMBOLD PROTEIN (VEINLET PROTEIN)
7337	20367	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	ba76403.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
7337	20367	34496	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBDG08 5'
8928	22007	36548	1.57	3.0E-10	H87208.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBDG08 5'
9249	22326	36872	1.52	3.0E-10	AW860731.1	EST_HUMAN	y674b12.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220611 3' similar to contains MER28 repetitive element:
9249	22326	36873	1.52	3.0E-10	AW860731.1	EST_HUMAN	IL3-CT0219-180200-064-B08 CT0219 Homo sapiens cDNA
9541	22606		0.78	3.0E-10	AF020503.1	NT	IL3-CT0219-180200-064-B08 CT0219 Homo sapiens cDNA
10878	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10820	23833		0.86	3.0E-10	AA766294.1	EST_HUMAN	yc11e12.f1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:30398 5'
12941	25619	31977	1.87	3.0E-10	BE175617.1	EST_HUMAN	rz38g03.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288908 3'
36	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	IL3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA
36	13274	26279	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1048	15089		1.66	2.0E-10	U80017.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
3051	16227		0.84	2.0E-10	BF675047.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
5824	19111		2.3	2.0E-10	Q28640	SWISSPROT	602136640.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	(HFRG)
7337	20610	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8203	21285	34807	0.58	2.0E-10	P26809	SWISSPROT	601686208.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34808	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8502	22558		1.06	2.0E-10	BF434565.1	EST_HUMAN	7c78408.x1 NCL CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11809	24682		1.33	2.0E-10	A1882153.1	EST_HUMAN	la10f12.x1 Soares total fetus NE2-1F8 9w Homo sapiens cDNA clone IMAGE:2043695 3'
1638	14691		3.09	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-280300-001-001 SN0038 Homo sapiens cDNA
1637	14769	27674	3.37	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2949	15772		2.16	1.0E-10	AW652001.1	EST_HUMAN	QV0-CT0225-191189-058-608 CT0225 Homo sapiens cDNA
3589	16753	29768	0.9	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-181189-019-g10 TT0003 Homo sapiens cDNA
3929	16793		0.87	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.78	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.93	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30378	18.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), GDM protein (GDM), adrenoleukodystrophy protein >
4245	17391	30379	18.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), GDM protein (GDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Homo sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
4265	17430		2.28	1.0E-10	M30628.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5277	18398		1.01	1.0E-10	A1797745.1	EST_HUMAN	Human sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
7044	20713		0.58	1.0E-10	P08548	SWISSPROT	WER31.1 MER31 repetitive element
7880	20914	34419	0.89	1.0E-10	AU128594.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8434	21515	35046	1.14	1.0E-10	AW408990.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5'
8855	21934		1.82	1.0E-10	A1268340.1	EST_HUMAN	fb 6A4 Fetal brain library Homo sapiens cDNA
10408	23441		6.24	1.0E-10	AA081888.1	EST_HUMAN	qim04610.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
11154	24225	37854	3.5	1.0E-10	A038280.1	EST_HUMAN	zn23g08.r1 Stratiogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
12165	18503		1.8	1.0E-10	X87344.1	NT	cy65h03.x1 Soares fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:1672681 3'
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	HL.sapiens DMA, DMB, HLA-Z1, IFF2, LMP2, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	IL2-IT0203-291089-018-c08 HT0203 Homo sapiens cDNA
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: h1ar1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: h1ar1) Homo sapiens cDNA clone DKFZp547D225 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	28657	2.98	9.0E-11	AL134396.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3470	16637	28658	2.98	9.0E-11	AL134396.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
4622	17759	30741	0.8	9.0E-11	AA778985.1	EST_HUMAN	aa78901.s1 Strategene echino brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5692	18888		3.05	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324980.1	EST_HUMAN	ESTZ7872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324980.1	EST_HUMAN	ESTZ7872 Cerebellum II Homo sapiens cDNA 5' end
12558	25378	32072	2.45	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human acrla polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-606808 5'
3185	16360		10.53	8.0E-11	H18971.1	EST_HUMAN	Yns3911.s1 Sources adult brain N2b5H55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	Yw46e08.s1 Wetzmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5913	19101	32415	0.66	8.0E-11	AW674916.1	EST_HUMAN	ba6004.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900882 3'
6811	19905		0.62	8.0E-11	AW166158.1	EST_HUMAN	Xf45h11.x1 NCI_CGAP_Brm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11 MER10 repetitive element;
1478	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
8695	21776	35307	2.61	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10434	23469		1.37	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
426	19820	26887	6.19	8.0E-11	M55270.1	NT	ENDONUCLEASE
426	19820	26882	6.19	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
6862	20014	33424	0.91	6.0E-11	L44140.1	NT	Human matrix Gla protein (MGF) gene, complete cds
7870	20924	34431	3.6	6.0E-11	P08547	SWISSPROT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
8559	21840	33179	6.99	6.0E-11	AV727850.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	AV727850 HTC Homo sapiens cDNA clone HTCCSC06 5'
12	13250	26250	1	5.0E-11	AL163283.2	NT	GM6-BT0281-031198-087-e03 BT0281 Homo sapiens cDNA
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6545	19804	33181	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C083
7859	20764	34248	11.57	5.0E-11	11416709	NT	Homo sapiens chromosome 21 segment HS21C013
1433	14566		1.38	4.0E-11	AA496042.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
2851	15685	29074	9.94	4.0E-11	BE585900.1	EST_HUMAN	aa01b12.r1 Sources_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
3034	16210	29233	1.26	4.0E-11	AL163247.2	NT	601507631F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
4740	17875	30858	0.81	4.0E-11	D44668.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6805	19768	33154	3.29	4.0E-11	P20085	SWISSPROT	HUMSUJPY069 Human brain cDNA Homo sapiens cDNA clone 069
							PRE-MIRNA SPLICING FACTOR RNA HELICASE PRP2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33718	0.82	4.0E-11	AA442630.1	EST_HUMAN	z66f10.1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:757863 5' similar to TR: 1055250 G1055250 PHEROMONE RECEPTOR VN4.;
7532	20605		3.68	4.0E-11	AF224689.1	NT	Homo sapiens marinosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9595	22850		1.56	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0258-210700-073-008 HT0258 Homo sapiens cDNA 1882g12.x1 NCI_CGAP_Brt23 Homo sapiens cDNA clone IMAGE:2105630 3' similar to WIP-ZK353.1 CE00388;
9882	22902	36487	0.79	4.0E-11	A1609753.1	EST_HUMAN	MR0-GN0024-180900-008-H09 GN0024 Homo sapiens cDNA
10698	23892	37513	0.84	4.0E-11	BF367283.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12794	25530	32008	1.71	4.0E-11	11945732	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
1521	14674	27768	4	3.0E-11	6878077	NT	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
4397	17534		1.35	3.0E-11	AA308248.1	EST_HUMAN	q38c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element;
982	14165	27215	1.43	2.0E-11	A1160502.1	EST_HUMAN	Yg43e12.1 Soares Infant brain INB Homo sapiens cDNA clone IMAGE:35144 5'
1212	14379	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	Yg43e12.1 Soares Infant brain INB Homo sapiens cDNA clone IMAGE:35144 5'
1212	14379	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1844	14798	27880	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1844	14796	27881	4.44	2.0E-11	L17432.1	NT	Human endogenous retrovirus HERV-P-T47D
2823	15837	29047	1.09	2.0E-11	AF087913.1	NT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3266	16440	29461	5.56	2.0E-11	P10283	SWISSPROT	tm54c09.x1 NCI_CGAP_Krt11 Homo sapiens cDNA clone IMAGE:2161936 3'
3403	16573	29588	0.82	2.0E-11	A1478617.1	EST_HUMAN	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNA6-POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNA6-T1)
3448	16618	29634	0.67	2.0E-11	Q10473	SWISSPROT	Homo sapiens FRASB common fragile region, deoxynucleoside triphosphate hydrolase (FRIT) gene, exon 5 FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
3596	16760		1.01	2.0E-11	AF020508.1	NT	RC3-BT0316-170200-014-005 BT0316 Homo sapiens cDNA
3797	16958	29892	0.64	2.0E-11	P70213	SWISSPROT	Homo sapiens chromosome 21 segment HS21C027
4596	17704		1.07	2.0E-11	BE065537.1	EST_HUMAN	QV2-BT0258-281099-014-001 BT0258 Homo sapiens cDNA
4728	17863		0.8	2.0E-11	AL103227.2	NT	EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2- macroglobulin
5051	18179		1.85	2.0E-11	BE082558.1	EST_HUMAN	QV2-P T0073-280300-109-H08 PT0073 Homo sapiens cDNA
5142	18285	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	
6263	19437	32794	1.23	2.0E-11	AW877808.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6440	19607	32870	2	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.l1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW PR16_YEAST
7245	20425	33888	0.85	2.0E-11	BF592845.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
8068	21148		0.89	2.0E-11	P37072	SWISSPROT	787c03.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3442685 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10491	23626	37135	5.13	2.0E-11	Q13608	SWISSPROT	OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.08	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.84	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11375	24436	38095	1.84	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11408	24469	38133	1.4	2.0E-11	AA281856.1	EST_HUMAN	2s1804.l1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:685519 5'
12122	25102	38807	12.19	2.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	26105		1.85	2.0E-11	AA704195.1	EST_HUMAN	2f77e03.s1 Soares_fetal_liver_spleen_INF1L5_S1 Homo sapiens cDNA clone IMAGE:469824 3'
12328	26237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RC0-CH0027-210100-011-c01 CN0027 Homo sapiens cDNA
12354	26299	32115	2.15	2.0E-11	BF377869.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12641	25431		1.43	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25542		3.62	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	25767		2.5	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
683	13876	26909	1.57	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
806	13986	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27484	2.81	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
1528	14881		1.82	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2086	15235	28358	0.94	1.0E-11	P16288	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	15330	28455	3.89	1.0E-11	AF000573.1	NT	Homo sapiens homogenized 1,2-dioxygenase gene, complete cds
2229	15363	28492	1.1	1.0E-11	AA308918.1	EST_HUMAN	EST180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' and similar to EST containing Alu repeat
3588	16752	29787	0.95	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5447	18847	31625	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
							7857d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
5953	19139	32455	0.78	1.0E-11	BF222848.1	EST_HUMAN	MER10 repetitive element ;
8398	21477	35004	2.65	1.0E-11	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8781	21860	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	Y73d08.l1 Soares_infant brain IN1B Homo sapiens cDNA clone IMAGE:28168 5'
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8248	22326	36871	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-603 NN1149 Homo sapiens cDNA
10828	23680		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11508	24621	36302	2.02	1.0E-11	BF680078.1	EST_HUMAN	602164807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4265977 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADHP, Human fetal Brain Whole tissue Homo sapiens cDNA
3017	16183	28216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36832	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36833	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8539	22804		0.88	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-038-G12 BT0578 Homo sapiens cDNA
12408	25287		4.88	8.0E-12	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4783	17818	30905	1.57	7.0E-12	Q06804	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	36402	6.8	7.0E-12	AA704736.1	EST_HUMAN	Z23g01.s1 Scores: fetal_liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18	7.0E-12	D10473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.96	8.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HITFAWF08 5'
4488	17608	30586	9.28	6.0E-12	AA732516.1	EST_HUMAN	ntz8811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
5336	18449	31418	5.12	6.0E-12	AK59161.1	EST_HUMAN	(f85g12.x1 Scores: NSF_F8_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148438 3' similar to contains MER10.12 MER10 MER10 repetitive element;
9196	22274	35911	1.09	6.0E-12	AF003249.1	NT	Marone sarcofili myosin heavy chain FM3A (FM3A) mRNA, complete cds
8676	22637		1.81	6.0E-12	AAB47898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387688 similar to contains MER29.12
13205	25766		1.25	6.0E-12	AW885846.1	EST_HUMAN	MER29 repetitive element;
1008	14234	27283	2.37	5.0E-12	T06573.1	EST_HUMAN	RC4-OT0072-060400-012-111 OT0072 Homo sapiens cDNA
3477	16844	29683	1.28	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat3638208) Homo sapiens cDNA clone HFBVDV33
3821	16981	29884	7.44	5.0E-12	AJ271738.1	NT	tz42505.y1 NCI_CGAP_Bnf52 Homo sapiens cDNA clone IMAGE:2281217 5'
6145	19323	32688	6.13	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32687	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6820	19780	33168	9.96	5.0E-12	AW974780.1	EST_HUMAN	EST388850 MAGE resequences, MAGN Homo sapiens cDNA
7176	20052	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1616_s1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1616_s1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21505	35038	1.28	6.0E-12	AA033745.1	EST_HUMAN	z01g12.s1 Scores: fetal_heart, N14-H19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8867	21848		0.65	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0088-220300-011-507 OT0088 Homo sapiens cDNA
9195	22273		0.77	5.0E-12	AL078581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434J0428 5'
9308	22384	35836	2.52	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9023	22978	30247	1.22	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.69	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10793	23826	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	26505	3.29	4.0E-12	AA700326.1	EST_HUMAN	274911.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
255	13474	26505	3.42	4.0E-12	AA700326.1	EST_HUMAN	274911.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4742	17877	30860	0.88	4.0E-12	AI889884.1	EST_HUMAN	bc26105.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13639 MARINER TRANSPOSASE. ;
7787	20953		0.71	4.0E-12	BF445140.1	EST_HUMAN	rad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2 MER7 repetitive element ;
8437	21318		4.81	4.0E-12	AF109897.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11338	24401	38050	4.33	4.0E-12	AJ228043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21c22, segment 3/3
12884	25458		2.11	4.0E-12	U78077.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13816	26839	2.58	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517 O14517 SMRP. ;
631	13816	26840	2.58	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517 O14517 SMRP. ;
5278	18395	31363	0.78	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5568	18766	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8570	21651	35183	0.5	3.0E-12	O95453	SWISSPROT	SERINE PROTEASE HEPSIN
10891	23975	37606	2.32	3.0E-12	U37872.1	NT	Human prostate specific antigen gene, 5' flanking region
10891	23975	37607	2.32	3.0E-12	U37872.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27821	1.24	2.0E-12	AW802131.1	EST_HUMAN	IL5-LJM0071-120400-085-e05 UNK0071 Homo sapiens cDNA
3658	16721	28736	0.93	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4941	17679		2.09	2.0E-12	BE063509.1	EST_HUMAN	CHM-BT0281-031108-087-e03 BT0281 Homo sapiens cDNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
6808	19766		2.08	2.0E-12	AW971857.1	EST_HUMAN	EST1363946 MAGC resequences, MAGL Homo sapiens cDNA
7328	20408	33870	3.85	2.0E-12	T08169.1	EST_HUMAN	EST106060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7469	20674	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF186884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10191	23228		8.32	2.0E-12	BE165880.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.78	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Scores_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR-Q13538
12129	25109	38819	1.53	2.0E-12	AW242834.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN.
12313	25228		1.34	2.0E-12	AL183283.2	NT	nc27k03.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2864985 3'
12516	25352		1.46	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
125	13354	25385	1.64	1.0E-12	AW627874.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2044	15185		1.78	1.0E-12	AB71728.1	EST_HUMAN	h180408.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.H1
3138	16314	20326	1.04	1.0E-12	AF000891.1	NT	MER18 repetitive element.
3138	16314	28327	1.04	1.0E-12	AF000891.1	NT	wt51807.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
3978	17135	30138	40.43	1.0E-12	AU132248.1	EST_HUMAN	repetitive element:
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6088	19289		1.8	1.0E-12	U82828.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6188	19342		1.82	1.0E-12	Q8V237	SWISSPROT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6282	19455	32805	0.59	1.0E-12	BF642800.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
							Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
							HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
							EST000008 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							EST000008 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
6982	19821	33208	0.83	1.0E-12	AF228843.1	NT	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7265	20348	33800	2.53	1.0E-12	AF186884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							q168a04.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:184814 3' similar to
							gdxM18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.H1 MER10
							repetitive element:
7300	20382	33840	10.78	1.0E-12	AI248533.1	EST_HUMAN	q168a04.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:184814 3' similar to
							gdxM18503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.H1 MER10
7300	20382	33841	10.78	1.0E-12	AI248533.1	EST_HUMAN	repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8686	21766	35298	0.59	1.0E-12	U66059.1	NT	Human gamma T-cell receptor beta chain Dqamline-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S8/13S>
8902	21981	35521	1.25	1.0E-12	AA782323.1	EST_HUMAN	ac26605.s1 Strati gene ovary (8637217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25168	36835	2.92	1.0E-12	AW082164.1	EST_HUMAN	EST1374237 MAGE reassurances, MAGG Homo sapiens cDNA
12437	25310		1.54	1.0E-12	AI738592.1	EST_HUMAN	wk33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392085 3'
12600	25068		1.93	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12788	25168		1.19	1.0E-12	P44836	SWISSPROT	PROBABLE TONIB-DEPENDENT RECEPTOR H10712 PRECURSOR
12951	25561		2.82	1.0E-12	AF224693.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4050	17212	30223	1.21	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22941		2.81	9.0E-13	N09653.1	EST_HUMAN	za28808.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:293651 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	15029	28136	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34608	0.63	8.0E-13	AI894398.1	EST_HUMAN	wm31h08.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437801 3'
8303	21385	34607	0.63	8.0E-13	AI894398.1	EST_HUMAN	wm31h08.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437801 3'
10350	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21610		0.77	7.0E-13	Q06166	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	501463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866513 5'
12976	25635		1.53	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
2168	15303	28430	5.65	8.0E-13	AL163207.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNACTOPOLYPEPTIDE, N-
5239	18361	31329	0.93	6.0E-13	AJ267928.1	EST_HUMAN	ac26605.s1 Strati gene ovary (8637217) Homo sapiens cDNA clone IMAGE:857577 3'
3399	18509		1.15	5.0E-13	R78338.1	EST_HUMAN	wk33h08.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437801 3'
3484	16652		1.56	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728360 3' similar to contains Alu
7016	20162	33572	0.99	5.0E-13	P08083	SWISSPROT	repetitive element/contains element MER22 repetitive element ;
11100	24173	37808	2.84	5.0E-13	P07313	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
1016	15059		4.88	4.0E-13	AW378014.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
							PM2-HT0224-221069-001-011 HT0224 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15558		1.61	4.0E-13	AF03529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
4880	18002		1.06	4.0E-13	AA454054.1	EST_HUMAN	z48807.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785469 5'
5704	18887	32180	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33856	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	z478g12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7898	20850		2.82	4.0E-13	AA4291.1	EST_HUMAN	y933g05.1 Soares_melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR-A32895
8042	22121	35683	1.38	4.0E-13	AL043810.1	EST_HUMAN	A32895 t complex sterility protein - mouse
9702	22751	36321	0.47	4.0E-13	AA076807.1	EST_HUMAN	DKF7p434A0128_11 434 (synonym: hba3) Homo sapiens cDNA clone DKF7p434A0128 5'
10228	23262	36850	4.44	4.0E-13	AL289831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	q182d05.x1 NCJ CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	repetitive element
184	13406		4.95	3.0E-13	AF03528.1	NT	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
1802	14855	27737	0.96	3.0E-13	AB04181.1	EST_HUMAN	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
2443	15571	28700	1.83	3.0E-13	AJ271738.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2648	15673		2.28	3.0E-13	AL163210.2	NT	z488g08.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2729	15847	28957	3.89	3.0E-13	BF372982.1	EST_HUMAN	CM-BT043-080209-075 BT043 Homo sapiens cDNA
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
3862	16756	29771	9.73	3.0E-13	P18816	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
3902	16756	29772	9.73	3.0E-13	P18816	SWISSPROT	CM3-F10100-140700-242-H08 FT0100 Homo sapiens cDNA
5657	18851	32133	0.88	3.0E-13	AA134017.1	EST_HUMAN	cb18d02.s1 NCJ CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
5657	18851	32134	0.88	3.0E-13	AA134017.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
6114	19294	32829	0.73	3.0E-13	AW005639.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
8057	21149	34868	7.1	3.0E-13	U52111.2	NT	z488h10.1 Stratiogene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:585315 5' similar to contains THR.12 THR repetitive element
						EST_HUMAN	z488h10.1 Stratiogene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:585315 5' similar to contains THR.12 THR repetitive element
						EST_HUMAN	wz88c02.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565860 3' similar to TR:O75139
						EST_HUMAN	O75139 KIAA0644 PROTEIN ;
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	21350	34865	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Reactive factor
8268	21350	34866	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Reactive factor
10401	23436	37043	0.58	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23038		3.1	3.0E-13	AD64768.1	EST_HUMAN	HAC536 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE069508.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11888	24886	38585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
154	13379	28411	3.52	2.0E-13	U52111.2	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
249	13470	28502	2.06	2.0E-13	U23839.1	NT	
1289	14455	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16246	28266	0.61	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16246	28267	0.61	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3596	16760	29776	1.68	2.0E-13	AF108807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		0.58	2.0E-13	X79417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6964	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7169	20064	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristyltransferase 1 (NMT1), mRNA
7169	20064	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristyltransferase 1 (NMT1), mRNA
10675	23709	37317	2.41	2.0E-13	5031806	NT	Homo sapiens mab-21 (G. elegans)-like 1 (MAB21L1) mRNA
12388	25274		22.49	2.0E-13	AW932153.1	EST_HUMAN	CM0-HN0001-100390-274-e11 HN0001 Homo sapiens cDNA
302	13518	26551	1.34	1.0E-13	S74128.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AL007973.1	NT	Homo sapiens LGMD2B gene
							H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1367	14521	27596	1.4	1.0E-13	X87944.1	NT	
2079	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.e1 NCL CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR3 THR repetitive element:
4715	17950	30853	1.32	1.0E-13	BF340987.1	EST_HUMAN	602038002F1 NCL CGAP_Btm84 Homo sapiens cDNA clone IMAGE:4185568 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8094	21178	34891	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element;
8094	21178	34892	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element;
10285	23330		1.04	1.0E-13	O15461	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11961	24740	38431	6.74	1.0E-13	BF108755.1	EST_HUMAN	744610.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12208	25160		1.38	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12920	26605		3.48	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13077	25706		1.85	1.0E-13	X87578.1	NT	H. sapiens CD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2569	15994		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	28036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	28360	7.5	9.0E-14	AW513286.1	EST_HUMAN	xs54h05.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3698	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	18010	30994	2.23	9.0E-14	AJ002153.1	NT	Sequitus oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE468263.1	EST_HUMAN	h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4068	17222		3.84	8.0E-14	R76289.1	EST_HUMAN	yf72e03.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
9047	21090	34805	38.93	8.0E-14	X86211.1	NT	H. sapiens DNA for endogenous retroviral like element
9760	22698	36268	3.22	8.0E-14	AA219318.1	EST_HUMAN	za17c10.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628970 3'
11717	24767		1.79	8.0E-14	BE062568.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	A1698118.1	EST_HUMAN	ws82h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1658	18044		4.76	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
9120	22169		0.73	7.0E-14	AL163285.2	NT	MER10 repetitive element;
							Homo sapiens chromosome 21 segment HS21C085
378	13588	26620	12.43	6.0E-14	AF026003.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHTT) gene, exon 5

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10027	23065	36682	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRASB common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10027	23065	36683	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRASB common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
633	13918	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
6168	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	x603605.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2875185 3' similar to contains L1.12 L1 repetitive element;
5650	18944	32125	5.28	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	16030		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1928	15089	28174	10.15	4.0E-14	AJ007873.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	AA046502.1	EST_HUMAN	z667a00.1 Scores_pregnant_uterus_NbrHPU Homo sapiens cDNA clone IMAGE:487898 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	yf73c12.e1 Scores_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:278160 3' similar to contains L1.13 L1 repetitive element;
8145	21227		0.71	4.0E-14	X87344.1	NT	H. sapiens DMA, DMB, HLA-z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12043	25024	38729	5.5	4.0E-14	BE242468.1	EST_HUMAN	TCAAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1470
12866	26203		5.69	4.0E-14	AB888224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_UH4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
972	14145	27204	1.58	3.0E-14	X95498.1	NT	R. norvegicus mRNA for GPG2 protein
6873	20025	33434	0.93	3.0E-14	AA020786.1	EST_HUMAN	f691g12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 000519 FATTY ACID AMIDE HYDROLASE.;
6873	20025	33435	0.93	3.0E-14	AA020786.1	EST_HUMAN	f691g12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 000519 FATTY ACID AMIDE HYDROLASE.;
7173	20306	33749	0.6	3.0E-14	AA386311.1	EST_HUMAN	EST168054 Brain IV Homo sapiens cDNA
8987	22066	35608	0.86	3.0E-14	N42165.1	EST_HUMAN	yv07b10.1 Scores_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
11512	18495	31533	5.87	3.0E-14	AW263354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_JNY11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12804	26041		1.88	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
13212	25894	31853	1.51	3.0E-14	BE891660.1	EST_HUMAN	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920189 5'
401	13598	26634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
708	16019	26825	11.98	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2491	15588		1.04	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0377-081289-031-D12 BT0377 Homo sapiens cDNA
2835	15680		0.96	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2893	15718	28835	1.03	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
5641	18835	31812	0.97	2.0E-14	BF380681.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18831	32229	1.03	2.0E-14	A312351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:20507225 3' similar to contains L1.3 L1 repetitive element;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20189		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P66163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7678	20741	34221	24.48	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7678	20741	34222	24.48	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.56	2.0E-14	A976795.1	EST_HUMAN	w58g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23684	37273	0.51	2.0E-14	AV74164.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone C8FB8F04 5'
11019	24098	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	UIH-B1-adw-e-10-Q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G8 protein (GR6) gene, complete cds
13163	15680		1.26	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1062	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14581	27684	7.01	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14581	27685	7.01	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	15198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filament (FLN) gene to glucose-6-phosphate dehydrogenase ((G6PD) gene, complete cds
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001688.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	28210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	28424	3.14	1.0E-14	BF35227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	28425	3.14	1.0E-14	BF35227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3692	17149	30155	1.69	1.0E-14	AA682984.1	EST_HUMAN	ae88c12.s1 Strabagana schizoa brain S11 Homo sapiens cDNA clone IMAGE:871350 3'
4596	17733	30713	2.01	1.0E-14	AW276862.1	EST_HUMAN	xp39h10.x1 NCI_CGAP_L1281 Homo sapiens cDNA clone IMAGE:2753059 3'
5930	19116	32429	1.98	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6813	26834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6813	26834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
1607	14760	27839	1.81	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	16376		1.38	9.0E-15	AF106779.1	NT	Homo sapiens transcription factor K3H11 protein, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
7666	20732	34207	4.24	8.0E-15	P21410	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P16, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE003599.1	EST_HUMAN	601077750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980159 5'
13099	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
7307	20412	33874	1.19	7.0E-15	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
10650	23894		2.34	7.0E-15	AW241093.1	EST_HUMAN	bcn71402.x1 Sources_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element:
12270	25203		1.44	7.0E-15	AA284465.1	EST_HUMAN	zs57608.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:U121894 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.11 L1 repetitive element:
1018	14180	27250	7.51	8.0E-15	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
5283	18382		0.98	6.0E-15	AW601288.1	EST_HUMAN	GM4-NN1011-100300-110-d10 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11683	26231		1.54	6.0E-15	AW838843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13618	26658	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2818	15933	28044	1.79	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, R4Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
440	13240	28240	2.33	4.0E-15	AL163303.2	NT	ENDONUCLEASE]
6804	19959	33359	0.9	4.0E-15	AB007970.1	NT	Homo sapiens chromosome 21 segment HS21C103
11316	21095	34577	2.11	4.0E-15	AJ130884.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21095	34578	2.11	4.0E-15	AJ130884.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.57	3.0E-15	N89452.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
5141	18264	31232	0.57	3.0E-15	AA078097.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIOLIPIN)
5141	18264	31233	0.57	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.17	3.0E-15	Q64625	SWISSPROT	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7430	20507	33978	3.13	3.0E-15	M27685.1	NT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33979	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20507	33979	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10126	23167		2.36	3.0E-15	AA807128.1	EST_HUMAN	cc36d07.s1 NCI_OGAP_GC81 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element:
11033	24112	37748	8.11	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
260	13479	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
378	13587	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1509	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3509	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3509	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17880		2.76	2.0E-15	AB060335.1	EST_HUMAN	wf07709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TRQ81049 Q61043 NINEIN.;
6311	19483	32838	1.11	2.0E-15	BE662352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6311	19483	32839	1.11	2.0E-15	BE662362.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7263	20349		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, OEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20498	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	z177603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:400924 3'
7654	20628	34102	5.05	2.0E-15	W05084.1	EST_HUMAN	z177610.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:400924 3'
9107	22186	35730	2.86	2.0E-15	D14847.1	NT	WP:144F4.8 CE02227 TRANSPOSASE;
9273	22349	35899	0.91	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9273	22349	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	z177608.r1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:728414 5'
9804	22659	36231	1.18	2.0E-15	AW379465.1	EST_HUMAN	z177608.r1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:728414 5'
9804	22659	36232	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201089-078-e12 HT0244 Homo sapiens cDNA
11077	24152		3.69	2.0E-15	AJ271735.1	NT	CM0-HT0244-201089-078-e12 HT0244 Homo sapiens cDNA
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13016	16783	29779	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948		3.08	1.0E-15	AI688984.1	EST_HUMAN	bc28h05.x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR-Q19639 Q19639
3077	16253	29275	1.42	1.0E-15	BE043584.1	EST_HUMAN	MARINER TRANSPOSASE. ;
3211	16385	29398	1.18	1.0E-15	P08547	SWISSPROT	IK40602.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2889162 5'
4479	17819	30601	0.81	1.0E-15	BE182688.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6502	19888	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	RC3-H10849-100500-022-005 HTD849 Homo sapiens cDNA
7149	20284		1.98	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.a1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7184	20048	33460	0.78	1.0E-15	P39057	SWISSPROT	MER8 repetitive element ;
8427	21508	35040	0.99	1.0E-15	AL163280.2	NT	QV3-BT0568-270100-074-g05 BT0568 Homo sapiens cDNA
8816	21896	35232	4.94	1.0E-15	AL200976.1	EST_HUMAN	DYNEIN BETA CHAIN, CILIARY
8815	21895	35233	4.94	1.0E-15	AL200978.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8239	22316	36858	0.78	1.0E-15	AL163207.2	NT	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8242	22319	36862	0.98	1.0E-15	4507208	NT	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9448	22594	36127	0.99	1.0E-15	Q39575	SWISSPROT	Homo sapiens chromosome 21 segment HS21C007
9832	22872	36455	0.94	1.0E-15	AA864653.1	EST_HUMAN	Homo sapiens spermidine synthase (SRM) mRNA
11057	24134	37770	3.04	1.0E-15	AF044083.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
13104	25992	31856	13.05	1.0E-15	AI783944.1	EST_HUMAN	ch37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.8 L1
4828	17762	30744	0.93	9.0E-16	4503168	NT	Homo sapiens major histocompatibility locus class III region
11241	24310	37847	1.41	9.0E-16	F08688.1	EST_HUMAN	repetitive element ;
11885	24880	38885	1.48	9.0E-16	AI244341.1	EST_HUMAN	IC31C05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element
11885	24980	38886	1.48	9.0E-16	AI244341.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAAAT displacement protein)(CUTL1) mRNA
5819	19009	32315	0.85	7.0E-16	4885120	NT	H8C23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05
7486	20571	34043	1.3	7.0E-16	O88807	SWISSPROT	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868354 3' similar to contains MER10.13
7498	20571	34044	1.3	7.0E-16	O88807	SWISSPROT	MER10 repetitive element ;
19043	25895		38.08	7.0E-16	T84149.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868354 3' similar to contains MER10.13
							MER10 repetitive element ;
							Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV)(PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV)(PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							ye28c12.l1 Stratiogene lung (4837210) Homo sapiens cDNA clone IMAGE:118082 5'

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2208	15342		9.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE:ressequenc, MAGL Homo sapiens cDNA
1522	14875	27757	0.86	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA922178.1	EST_HUMAN	cd80c04.s1 Soares total_fetus_Nb21F8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11809	24709	38498	2.68	5.0E-16	BF217388.1	EST_HUMAN	contains element L1 repetitive element:
13152	25749		14.16	5.0E-16	11418127	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2312	15444		1.01	4.0E-16	AB001623.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2463	15581	28708	2.87	4.0E-16	AW787168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2453	15581	28708	2.87	4.0E-16	AW787168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3546	16711	29722	5.29	4.0E-16	Q16633	SWISSPROT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4280	17405	30391	8.68	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4280	17405	30392	6.68	4.0E-16	BE083875.1	EST_HUMAN	PMA-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	PMA-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9495	22552	36114	0.72	4.0E-16	11423181	NT	Homo sapiens chromosome 21 segment HS21C084
12393	25218		1.95	4.0E-16	P08548	SWISSPROT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12381	25270		8.68	4.0E-16	C05947.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12392	25277	32079	3.23	4.0E-16	6912469	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12682	25454		1.33	4.0E-16	R18591.1	EST_HUMAN	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	y186b11.t1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26396	1.08	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
478	13873		1.58	3.0E-16	AL046445.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
488	13982		2.33	3.0E-16	AF135448.1	NT	DKFZp434P037.t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434P037 5'
1483	14836	27720	2.73	3.0E-16	Q28983	SWISSPROT	Homo sapiens TSX (TSX) pseudogene, exon 5
						SWISSPROT	ZONADHESIN PRECURSOR
						SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN
3041	16217	28237	4.71	3.0E-16	P03200	SWISSPROT	GP220]
4711	17846	30830	0.59	3.0E-16	AW160828.1	EST_HUMAN	au178b08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2762163 5' similar to
5057	16185	31160	1.32	3.0E-16	AY661393.1	EST_HUMAN	SW-KID1_MOUSE Q81751 RENAL TRANSCRIPTION FACTOR KID-1;
5392	18394		0.89	3.0E-16	AA077225.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCOSA01 3'
5734	18927	32223	1.67	3.0E-16	AF003529.1	NT	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
						EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
						EST_HUMAN	am98h05.s1 Strategene scRNA brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
8858	21837	35473	4.25	3.0E-16	AI002836.1	EST_HUMAN	TI-RB2 THR repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	BF690617.1	EST_HUMAN	60224633BF1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36968	2.59	3.0E-16	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	26171	31557	3.62	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434L1623 5'
904	14168		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2459	15598		0.96	2.0E-16	AA621761.1	EST_HUMAN	af06cd04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2753	15870		1.14	2.0E-16	J03061.1	NT	Human SSAN-related endogenous retroviral LTR-like element
4294	17437	30424	1.92	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	AL208733.1	EST_HUMAN	cg56003.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839187 3' similar to contains MER28.13
5269	18416	31385	0.64	2.0E-16	BE061176.1	EST_HUMAN	MER29 repetitive element;
6880	20032	33442	0.68	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-131189-003-H12 BT0046 Homo sapiens cDNA
7683	20945	34451	0.98	2.0E-16	AA70723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							g16e11.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
8154	21236	34757	1.57	2.0E-16	AF32837.1	EST_HUMAN	nz4706.x5 NCJ_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849
8352	21433	34957	0.81	2.0E-16	BE658026.1	EST_HUMAN	HYPOPHETICAL 42.9 KD PROTEIN, [2] TR:O08905; contains MER7.11 MER7 repetitive element;
8352	21433	34958	0.81	2.0E-16	BE658026.1	EST_HUMAN	782h08.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.78	2.0E-16	AW877214.1	EST_HUMAN	782h08.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35341	0.78	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	AF200719.1	NT	GM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
383	13630		22.93	1.0E-16	AA628592.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
2028	15169	28276	3.42	1.0E-16	BF327942.1	EST_HUMAN	af39g11.s1 Soares testis_NHT testis_NHT2-IF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to
5839	18028	32335	0.6	1.0E-16	AF163884.1	NT	contains ORF.12 ORF repetitive element;
6565	19727		18	1.0E-16	U45983.1	NT	QV6-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
6704	19862	33252	2.96	1.0E-16	Q02779	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7726	19727		5.39	1.0E-16	U46983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKOR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3832	16962	26994	2.08	9.0E-17	AW800048.1	EST_HUMAN	GM1-NIN1003-200300-163-a01 NIN1003 Homo sapiens cDNA
6884	20016		2.15	9.0E-17	AI392984.1	EST_HUMAN	ig22c11.x1 NCJ_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2108524 3' similar to contains MER28.12
							MER28 repetitive element;

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8288	21381		3.56	9.0E-17	AW160287.1	EST_HUMAN	xq49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains ORF.12 OFR repetitive element;
10429	23484		2.35	9.0E-17	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3968	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-080300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV780769.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1487	14840		2.58	7.0E-17	6753087	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5438	18638		3.11	7.0E-17	AF210850.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6828	19979	33387	7.91	7.0E-17	AF220843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
208	13431	28463	5.82	6.0E-17	AW883880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
6443	19810	32973	2.06	8.0E-17	AW682772.1	EST_HUMAN	h81004.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878595 3' similar to contains L1.12 L1 repetitive element;
10499	23534	37144	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
434	13234	28234	2.37	5.0E-17	T84110.1	EST_HUMAN	yc05h08.l1 Strabagene lung (#837210) Homo sapiens cDNA clone IMAGE:79839 5'
7759	20818	34308	1.81	6.0E-17	T81043.1	EST_HUMAN	y428h04.l1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9582	22704	38270	1.32	4.0E-17	AW128165.1	EST_HUMAN	px20h04.x1 NCI_CGAP_Ki68 Homo sapiens cDNA clone IMAGE:2818822 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11783	24773	39469	2.51	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12308	25236		1.82	4.0E-17	AD79548.1	EST_HUMAN	ov45h04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR.Q16530
2165	15300	28426	1.85	3.0E-17	AW118123.1	EST_HUMAN	O18530 PMS3 mRNA; contains MER10.12 MER10 repetitive element;
3263	16437		1.17	3.0E-17	P36410	SWISSPROT	pd88h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3732	16893	28887	1.91	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	16893	28898	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05h04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181988 3'
						EST_HUMAN	hw05h04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181988 3'
8463	21644	35074	1.12	3.0E-17	N68451.1	EST_HUMAN	zai14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.13 PTR5 repetitive element;
8903	22943	36528	5.19	3.0E-17	AB020898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-e12 BN0047 Homo sapiens cDNA
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-e12 BN0047 Homo sapiens cDNA
12288	25201		4.2	3.0E-17	11417988	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLC01F08 5'
383	13574	28605	2.05	2.0E-17	AL270080.1	EST_HUMAN	q83a08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1868922 3' similar to contains Alu repetitive element
384	13574	28605	2.78	2.0E-17	AL270080.1	EST_HUMAN	q83a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1868922 3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA722832.1	EST_HUMAN	z881d04.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:389751 3'
2518	15844	28766	2.58	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518	15844	28766	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2886	18172	28191	6.98	2.0E-17	P12038	SWISSPROT	NEUROFILAMENT TRIPLET-H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31696	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31697	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
8394	18683		1.92	2.0E-17	AF055068.1	NT	Homo sapiens MHC class 1 region
6818	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610.J1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8008	21058	34588	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8276	21357	34875	1.24	2.0E-17	Q95158	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' and similar to similar to glycogenin
10073	23111	38715	2.71	2.0E-17	BE288888.1	EST_HUMAN	600844680F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:288888 5'
10108	23146	38744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23146	38745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10468	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10580	23825	37232	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10580	23825	37233	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23852	37261	0.93	2.0E-17	AF788902.1	EST_HUMAN	we94b04.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23852	37262	0.93	2.0E-17	AF788902.1	EST_HUMAN	we94b04.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	13960	28699	2.79	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1807	14956	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15642	28689	3.18	1.0E-17	U70410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
9557	16820		1.03	1.0E-17	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4258	17401		9.42	1.0E-17	R09942.1	EST_HUMAN	y50e07.J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6791	19946	33344	1.82	1.0E-17	AI185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6791	19946	33346	1.82	1.0E-17	AI185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7298	20322	33768	1.33	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101289-072-007 BT0263 Homo sapiens cDNA
10210	23246	36836	1.04	1.0E-17	AW998538.1	EST_HUMAN	QV3-BN0046-220300-128-c10 BN0046 Homo sapiens cDNA
11703	24700	36303	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE_SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747		3.05	6.0E-18	AI472187.1	EST_HUMAN	g88403.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3888	17045	30044	2.14	6.0E-18	4769977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26589	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10404.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gclL20868 60S
359	13570	26800	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10404.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gclL20868 60S
7601	20671	34145	1.09	7.0E-18	AW887642.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-003 OT0091 Homo sapiens cDNA
12826	13570	26589	10.85	7.0E-18	AW316976.1	EST_HUMAN	xx10404.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gclL20868 60S
12826	13570	26800	10.85	7.0E-18	AW316976.1	EST_HUMAN	xx10404.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gclL20868 60S
3367	16539	29652	1.23	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for gila-derived nexin/protease nexin I, enhancer region
4868	18001		3.99	6.0E-18	PE2181	SWISSPROT	PROTEIN GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGase C) (TGC)
8444	21525		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA
8543	21624	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	AB08258.1	EST_HUMAN	RC-BT166-020469-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	AB08258.1	EST_HUMAN	RC-BT166-020469-014 BT166 Homo sapiens cDNA
11389	24480	38124	3.63	6.0E-18	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24884	38351	1.89	6.0E-18	X87944.1	NT	H. sapiens DMA, DMB, HLA-Z1, IAPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12634	25364	32068	3.91	6.0E-18	U87629.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1171	14334	27980	12.48	5.0E-18	AI280214.1	EST_HUMAN	q985g11.x1 Soares_placenta_860weeks_2Nbl-IP860W Homo sapiens cDNA clone IMAGE:1863688 3'
4433	17573	30555	0.59	5.0E-18	10946905	NT	similar to contains Alu repetitive element;
5387	18589	31561	1.29	5.0E-18	AF087913.1	NT	Mus musculus gasdermin (Gsdm), mRNA
8917	21896	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
							MIR0-HT0161-221089-002-006 HT0161 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24282	37832	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24282	37833	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12676	25450		6.28	5.0E-18	AW067182.1	EST_HUMAN	MIR1-SN0036-060400-001-g11 SN0035 Homo sapiens cDNA
13063	25636		28.96	5.0E-18	AV050547.1	EST_HUMAN	AV050547 GLC Homo sapiens cDNA clone GLCGA02.3'
127	13355	26388	0.91	4.0E-18	BE044076.1	EST_HUMAN	hs36104.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.L8
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	MER29 repetitive element;
1754	14903	27898	52.02	4.0E-18	AA021814.1	EST_HUMAN	MER29 repetitive element;
1838	15081		1.05	4.0E-18	AT38592.1	EST_HUMAN	hs24f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28326
2274	16407	28538	1.26	4.0E-18	Q08430	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2274	16407	28537	1.26	4.0E-18	Q08430	SWISSPROT	wt33h08.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2382095 3'
3982	17051	30050	0.61	4.0E-18	AI081598.1	EST_HUMAN	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N-
5479	18678	31691	2.47	4.0E-18	AI017695.1	EST_HUMAN	ACETYLGLUCOSAMINYL TRANSFERASE) (BRANCHING ENZYME) (IGNT)
5479	18678	31692	2.47	4.0E-18	AI017695.1	EST_HUMAN	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N-
8028	21112		0.92	4.0E-18	AA746811.1	EST_HUMAN	ACETYLGLUCOSAMINYL TRANSFERASE) (BRANCHING ENZYME) (IGNT)
11264	24323	37984	7.59	4.0E-18	AA371807.1	EST_HUMAN	ar83b06.x1 Barstead colon HFLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
872	14048	27114	3.81	3.0E-18	AA814186.1	EST_HUMAN	repetitive element;
953	14126	27187	2.25	3.0E-18	BE089534.1	EST_HUMAN	EST T83633 Pituitary gland, subtraacted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to
4060	17216	30226	1.06	3.0E-18	AL163247.2	NT	EST containing O family repeat
8988	20196	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	cd23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RSS_HUMAN
11167	24238	37869	1.99	3.0E-18	BF218650.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6 ;
12832	26654	28512	4.55	3.0E-18	AW022015.1	EST_HUMAN	CMO-BT0680-210300-288-g07 BT0690 Homo sapiens cDNA
281	13480	28512	4.2	2.0E-18	AW836820.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
1176	14339		74.12	2.0E-18	BE256087.1	SWISSPROT	PM6-BN0081-100300-001-508 BN0081 Homo sapiens cDNA
3183	16368	28374	0.94	2.0E-18	Q38575	SWISSPROT	601864858F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103662 5'
							df81h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
							QV1-LT0036-160200-070-g07 LT0036 Homo sapiens cDNA
							60114562F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA888810.1	EST_HUMAN	ak53a07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408852 3' similar to TR:O14577
5623	18817	31888	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A08 FROM 7Q31, COMPLETE SEQUENCE. ;
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5988	19184		1.84	2.0E-18	BF347228.1	EST_HUMAN	Human DNA, SINE repetitive element
6284	19487	32820	0.91	2.0E-18	X60459.1	NT	G02021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158670 5'
6284	19487	32821	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32838	0.9	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6448	19615	32979	2.93	2.0E-18	AW685833.1	EST_HUMAN	IL3-PT0819-220700-222-G12 HT0019 Homo sapiens cDNA
7594	20685	34141	0.50	2.0E-18	AA457619.1	EST_HUMAN	h94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878984 3' similar to contains
8341	21422	34947	0.5	2.0E-18	BE439524.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10253	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	aa88d11.1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
10253	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	TR:G61834 G61834 POLYPEPTIDE PR77 ;
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	HTM1-180F1 HTM1 Homo sapiens cDNA
12031	25014	38716	4.46	2.0E-18	AW151289.1	EST_HUMAN	X67610.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12
12465	14339		12.67	2.0E-18	BE266087.1	EST_HUMAN	MER10 repetitive element ;
4537	17676		0.75	1.0E-18	T85408.1	EST_HUMAN	MER10 repetitive element ;
5471	18671	31651	2.84	1.0E-18	AV683405.1	EST_HUMAN	X67610.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	h833d08.x1 NCI_CGAP_K1212 Homo sapiens cDNA clone IMAGE:2875488 3' similar to contains THR.b3
5688	18882	32175	3.08	1.0E-18	D00099.1	NT	THR repetitive element ;
6584	19748	33128	1.31	1.0E-18	AL103280.2	NT	XG47609.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2830728 3' similar to contains MER8.b2
6637	21717	35254	1.05	1.0E-18	AH148288.1	EST_HUMAN	MER8 repetitive element ;
10103	23141	36740	4.83	1.0E-18	U61328.1	NT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
12416	25284	32084	4.65	1.0E-18	AF003528.1	NT	ye43g05.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120636 5' similar to contains
							L1 repetitive element ;
							AV683405 G1C Homo sapiens cDNA clone GLCDKE11 3'
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens chromosome 21 segment HS21C080
							cd86d09.x1 Soares_sarcomat_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1880593 3' similar to
							contains L1.H1 L1 repetitive element ;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RbRat gene, and sodium phosphate transporter (NPTs) gene, complete cds
							Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	28780	5.1	9.0E-19	AA281981.1	EST_HUMAN	z11408.l1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
560	13752	28780	3.91	9.0E-19	AA281981.1	EST_HUMAN	z11408.l1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8032	21115		3.69	9.0E-19	F09688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8888	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8888	21965	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24453	38116	3.15	9.0E-19	AB032988.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13752	28780	19.34	9.0E-19	AA281981.1	EST_HUMAN	z11408.l1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1073	14239		1.68	8.0E-19	AW674802.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158988.1	EST_HUMAN	MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA
2319	15451	28583	1.74	7.0E-19	4758139	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6585	19747	33129	2.11	7.0E-19	AF082090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	A1344951.1	EST_HUMAN	h01608.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	26183		1.72	7.0E-19	AA705684.1	EST_HUMAN	z160301.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3879	17038		1.16	6.0E-19	AW852830.1	EST_HUMAN	PMO-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA
4685	17722	30706	1.66	8.0E-19	P34886	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34886	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	8.0E-19	AJ271795.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5978	19163	32483	5.17	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC56)
6346	19616	32873	0.59	5.0E-19	AW683302.1	EST_HUMAN	hh77808.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2668787 5'
10639	23673	37283	-1.18	6.0E-19	AJ287698.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38508	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87802.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element;
13083	25885		1.34	5.0E-19	U68060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S9A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12
588	13760	28784	0.86	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15864	28976	1.15	4.0E-19	BF687382.1	EST_HUMAN	602130910F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287674 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224889.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30526	0.85	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)
4400	17543	30527	0.85	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)
4589	17707	30888	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18596		0.89	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
							Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC33222), mRNA
7643	20615		1.88	3.0E-19	11432214	NT	Mus musculus mRNA for TPCR33 protein
9658	21101	34614	1.09	3.0E-19	X89685.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
12593	25395		16.36	3.0E-19	AF165520.1	NT	Homo sapiens chromosome 21 segment HS21C001
2627	15750	28665	20.06	2.0E-19	AL163201.2	NT	q81e02.X1 NCI CGAP_K415 Homo sapiens cDNA clone IMAGE:191588 3' similar to TR:Q69386 Q69386
4598	17706		1.34	2.0E-19	AB111783.1	EST_HUMAN	POUENF GENE;
6179	19355	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63	2.0E-19	7857286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8526	21606	35145	10.24	2.0E-19	AA012854.1	EST_HUMAN	zs84c09.t1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36753	0.84	2.0E-19	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13699		1.86	1.0E-19	BE408611.1	EST_HUMAN	G0130412F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3698310 5'
							yo79g07.t1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2233	15397	28486	1.84	1.0E-19	H30795.1	EST_HUMAN	MER10 repetitive element;
2782	15936		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	16087		6.72	1.0E-19	47588977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16655	28989	1.18	1.0E-19	AA894987.1	EST_HUMAN	q48b012.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1983631 3' similar to contains MER37.2
5452	18852	31631	0.73	1.0E-19	AJ890968.1	EST_HUMAN	MER37 repetitive element;
6189	19374	32725	2.6	1.0E-19	U12186.1	NT	wm9108.X1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16630 Q16630
6337	28213		0.63	1.0E-19	AA595527.1	EST_HUMAN	PMS3 MRNA;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	nm22d03.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:963068 similar to contains L1.H L1
7977	25856		0.75	1.0E-19	AF200719.1	NT	Oryctolagus cuniculus Nax-glucose cotransporter-related protein mRNA, complete cds
							Oryctolagus cuniculus Nax-glucose cotransporter-related protein mRNA, complete cds
							Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21724	35281	1.94	1.0E-19	MB4657.1	NT	Rabbit phosphatase kinase beta subunit mRNA, complete cds
8839	22018		2.72	1.0E-19	T89920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains
8850	22869		0.68	1.0E-19	U00322.1	NT	OPR repetitive element:
10300	23425	37032	25.12	1.0E-19	AW812289.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	RC0-STD174-181088-031405 ST0174 Homo sapiens cDNA
11184	24253	37888	1.87	1.0E-19	BE618026.1	EST_HUMAN	y31a03.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272872 5'
6784	19839	33338	2.4	8.0E-20	7657286	NT	601278882F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811483 5'
6784	19839	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7087	20752	34234	1.46	8.0E-20	A1221371.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7087	20752	34235	1.46	8.0E-20	A1221371.1	EST_HUMAN	cg89f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	16821	29637	0.71	7.0E-20	BF328456.1	EST_HUMAN	cg89f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7134	18500	31474	5.66	7.0E-20	AL138120.1	EST_HUMAN	PMA-ANO038-050300-003-004 ANO038 Homo sapiens cDNA
8893	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	DKFZp47D0882.r1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	nf48c04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
12014	24958		2.89	7.0E-20	6812633	NT	MER29 repetitive element:
3845	16808	28822	3.94	6.0E-20	P38188	SWISSPROT	nf48c04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
4367	17630	30511	4.58	6.0E-20	BE622434.1	EST_HUMAN	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
7264	20347	33789	1.42	5.0E-20	AF076301.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
8131	21213	34733	6.96	5.0E-20	W90525.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
8131	21213	34734	6.96	5.0E-20	W90525.1	EST_HUMAN	AF076301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8295	21377	34888	0.79	5.0E-20	BE165880.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element:
8035	22114	35657	1.28	5.0E-20	AB028174.1	NT	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element:
8035	22114	35658	1.28	5.0E-20	AB028174.1	NT	MIR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
9044	21087		1.13	5.0E-20	CG0009	SWISSPROT	Mus musculus MMAN-g mRNA, complete cds
1049	14802	27889	0.94	4.0E-20	AL163247.2	NT	Mus musculus MMAN-g mRNA, complete cds
5765	18957		1.13	4.0E-20	Q89890	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
8110	21192		5.01	4.0E-20	AB14352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10717	23750	37357	1.13	4.0E-20	AW687488.1	EST_HUMAN	HISTONE H2B C (H2B/C)
							ts84g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283396 3'
							QV5-UT0043-090200-080-c04 DT0043 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17468	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 14
4747	17882	30864	1.08	3.0E-20	AA037618.1	EST_HUMAN	z336b12.s1 Soares pregnant uterus NIH-IPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10527	23562	37168	0.47	3.0E-20	BF168284.1	EST_HUMAN	601843661F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4084343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
12331	26239	32109	0.09	3.0E-20	BE888422.1	EST_HUMAN	601614180F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	X224610.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5;
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng89h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:240097 similar to TR:G1224068
2878	14300		5.32	2.0E-20	AW303868.1	EST_HUMAN	G1224068 ORF2 FUNCTION UNKNOWN;
5061	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	ng89h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:240097 similar to TR:G1224068
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	G1224068 ORF2 FUNCTION UNKNOWN;
5256	18376		0.9	2.0E-20	5174538	NT	ng89h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:240097 similar to TR:G1224068
8309	21391	34915	0.97	2.0E-20	AA309467.1	EST_HUMAN	X224610.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
9391	22466	36030	2.65	2.0E-20	D10083.1	NT	X224610.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
9391	22468	36031	2.65	2.0E-20	D10083.1	NT	P97461 40S RIBOSOMAL PROTEIN S5;
12743	25878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	ZONADHESIN PRECURSOR
2070	15935	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	ZONADHESIN PRECURSOR
4580	17888	30679	1.02	1.0E-20	BF115193.1	EST_HUMAN	Homo sapiens male dehydrogenase 1, NAD (soluble) (MDH1) mRNA
7034	20170	33592	0.74	1.0E-20	AF049597.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' and
9394	22439	35998	2.08	1.0E-20	11418491	NT	Homo sapiens RGH1 gene, retrovirus-like element
11847	24638	38530	2.03	1.0E-20	AF223391.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
12461	25523		2.91	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
							CHR220310 Chromosome 22 even Homo sapiens cDNA clone C22_391 5'
							211406.J1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712611 5' similar to contains MER19.12
							MER19 repetitive element;
							hr4406.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
							repetitive element;
							AF049597 Human activated dendritic cell mRNA Homo sapiens cDNA clone GAO5
							Homo sapiens Autosomal Highly Conserved Protein (AHCN), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							nc89g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1
							repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2979	16156		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-8.121
12174	25135		3.98	9.0E-21	AW888188.1	EST_HUMAN	RC3-NIN0068-090503-021-b03 NIN0068 Homo sapiens cDNA
9011	22090		0.98	8.0E-21	AW674891.1	EST_HUMAN	b130a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11830	24919	38510	3.91	8.0E-21	AA808411.1	EST_HUMAN	C85109 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
12345	25250		3.8	8.0E-21	O21330	SWISSPROT	cd7106.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2130	15266	28385	3.85	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 8)
2130	16266	28386	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B8)
3792	16863	28958	1.36	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4369	17512		6.29	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6994	18728	33104	0.94	7.0E-21	AL163218.2	NT	z667a08.l1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:487858 5'
8592	21663	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C018
8876	21854	35490	4.94	7.0E-21	D14718.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-6
10319	23354	36863	1.07	7.0E-21	AW858922.1	EST_HUMAN	Human chromosomal protein HMGI1 related gene
10834	24016	37648	1.94	7.0E-21	AA723404.1	EST_HUMAN	RC0-CT0301-271189-031-F03 CT0301 Homo sapiens cDNA
4220	17359	30358	0.75	6.0E-21	BE408611.1	EST_HUMAN	z073403.s1 Soares_Fetal_Heart_NIH19W Homo sapiens cDNA clone IMAGE:398891 3' similar to
9336	22412		1.39	6.0E-21	BE162737.1	EST_HUMAN	gb:MI4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.L3 ORF
947	14120	27181	1.34	5.0E-21	5802031	NT	repetitive element ;
2354	15485	28817	1.23	5.0E-21	AA928194.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
4483	17623	30804	3.21	5.0E-21	BE068838.1	EST_HUMAN	PM1-HT0454-080100-002-b09 HT0454 Homo sapiens cDNA
4809	14120	27181	1.18	5.0E-21	5802031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4923	18053	31039	8.33	5.0E-21	4885474	NT	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541808 3' similar to TR:O02711
6902	20217		0.77	5.0E-21	AW440854.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
7157	20291	33734	1	5.0E-21	BE858505.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
10801	23834	37457	0.54	5.0E-21	Q91690	SWISSPROT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
10801	23834	37458	0.54	5.0E-21	Q91690	SWISSPROT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
12259	25195		1.28	5.0E-21	AA393574.1	EST_HUMAN	he05610.x1 NCI_CGAP_GML1 Homo sapiens cDNA clone IMAGE:2918154 3'
1772	14921	28015	1.88	4.0E-21	AA970713.1	EST_HUMAN	7834111.x1 NCI_CGAP_Py28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1
							OFR repetitive element ;
							ZINC FINGER PROTEIN GLI1 (GLI-1)
							ZINC FINGER PROTEIN GLI1 (GLI-1)
							z72041.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
							cc88a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16630
							PMS3 MRNA ; contains OFR.t1 ORF repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	20147	33568	2.61	4.0E-21	AB019578.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
6983	23022	36914	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRat gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36942	0.51	4.0E-21	AL163202.2	NT	Human sapiens chromosome 21 segment HS21C002
1894	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2248	15479	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3149	16324	29335	6.41	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5916	18910	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5916	18910	31879	0.82	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5959	19046		0.9	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone CLGGOA10 3'
6308	19480		2.74	3.0E-21	BF184738.1	EST_HUMAN	601844465F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4084945 5'
7215	20080	33493	7.52	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-018-g08 OT0083 Homo sapiens cDNA
9894	22834	36518	0.92	3.0E-21	AW687760.1	EST_HUMAN	CM1-NN0083-280400-203-h08 NN0083 Homo sapiens cDNA
12879	26089	31695	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
160	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0468-170200-090-g12 HT0468 Homo sapiens cDNA
939	14131	27189	0.51	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
939	14131	27190	0.51	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h06 BT0311 Homo sapiens cDNA
2703	15921	26937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15921	26938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18786	31846	1.66	2.0E-21	A1624992.1	EST_HUMAN	1s30f03.x1 NC1 CGAP_P an1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5694	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	HYPOPHYSICAL 51.1 KD PROTEIN;
5694	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	z997a12.r1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32679	0.74	2.0E-21	W44493.1	EST_HUMAN	z997a12.r1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:366910 5'
8467	21546	35078	0.58	2.0E-21	AJ010770.1	NT	z528h02.r1 Soares_sarcomatous_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323697 5'
8558	21639	35178	8.13	2.0E-21	BE141765.1	EST_HUMAN	Homo sapiens hypoxanthine gene, exons 1-50
9023	22102	35842	3.27	2.0E-21	AU136779.1	EST_HUMAN	QVQ-HT0103-081198-060-g11 HT0103 Homo sapiens cDNA
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11599	24652	38335	2.88	2.0E-21	BE373829.1	EST_HUMAN	H09g01.x1 NC1 CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
							601680836F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	2.0E-21	BE973829.1	EST_HUMAN	601680838F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	26388		6.44	2.0E-21	AF170816.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1284	14440	27509	1.89	1.0E-21	AA557657.1	EST_HUMAN	n48c04.s1 NCJ_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MIER20.b2
1484	14587		4.93	1.0E-21	AB01284.1	EST_HUMAN	MER28 repetitive element;
6816	19776		2.73	1.0E-21	AL079762.1	EST_HUMAN	ar88d12.x1 Barbead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
							DKFZp434f0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434f0830 5'
7342	20422	38885	4.7	1.0E-21	A1228104.1	EST_HUMAN	qq47a05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	PROTEIN (HUMAN);
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
13014	25687		1.67	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22 410-8
4590	17688	30654	2.38	9.0E-22	A1702438.1	EST_HUMAN	tx4a03.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266204 3' similar to TR:Q15408 Q15408
8803	21882	35420	2.02	9.0E-22	AL163201.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT;
8803	21882	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37746	3.1	9.0E-22	AV781874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
12007	24992	36696	1.39	9.0E-22	AU140358.1	EST_HUMAN	AV781874 MDS Homo sapiens cDNA clone MDS0005 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLAGE2 Homo sapiens cDNA clone PLACE2000394 5'
8080	21182		3.36	8.0E-22	AA046502.1	EST_HUMAN	CM0-HT0178-281089-078-h05 HT0178 Homo sapiens cDNA
682	13887	28898	3.78	7.0E-22	AL163246.2	NT	z67a06.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487853 5'
4398	17641	30522	3.27	7.0E-22	Q61838	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
5150	18272	31241	0.91	7.0E-22	AB008881.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
8888	21897		1.24	7.0E-22	AF151054.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8032	22111	35653	2.77	7.0E-22	M78590.1	EST_HUMAN	Homo sapiens HSPC220 mRNA, complete cds
9802	22842	38418	2.05	7.0E-22	AF009660.1	NT	EST00738 Fetal brain, Stratiogene (cat#838208) Homo sapiens cDNA clone HFBCF07
8436	21517		1.26	6.0E-22	AW029123.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
6846	19806	33192	3.27	6.0E-22	AL163203.2	NT	w05g07.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2842812 3'
10525	23550	37167	2.86	6.0E-22	U60822.1	NT	Homo sapiens chromosome 21 segment HS21C103
							Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12833	25555		1.63	5.0E-22	BF476511.1	EST_HUMAN	nea27a06.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu
3726	18897		0.77	4.0E-22	AJ271735.1	NT	repetitive element
8608	28224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10901	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	26672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14154		1.34	3.0E-22	AA69379.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2195611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element;
2836	15759	28873	1.33	3.0E-22	AB59038.1	EST_HUMAN	W66B04.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW_RL21_HUMAN
3783	18324		1.66	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.;
4922	18052	31038	3.18	3.0E-22	AB60125.1	EST_HUMAN	Human chromosomal protein HMGI related gene qb28c07.x1 Scores_pregnant_uterus_NhlPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8011	21061	34573	0.8	3.0E-22	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
8425	21508		1.11	3.0E-22	BE156613.1	EST_HUMAN	ENDONUCLEASE
8430	21611	35042	1.88	3.0E-22	BE080841.1	EST_HUMAN	QV0-HT0368-080200-099-112 HT0368 Homo sapiens cDNA
8555	21638	35172	1.14	3.0E-22	X60680.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	21638	35173	1.14	3.0E-22	X60680.1	NT	R radius RY205 mRNA for a potential ligand-binding protein
2009	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	R radius RY205 mRNA for a potential ligand-binding protein
2590	15716	28833	1.72	2.0E-22	P24916	SWISSPROT	yk73d05.s1 Scores melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:267369 3'
3507	18674	29684	3.98	2.0E-22		SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
4341	17484	30488	1.41	2.0E-22	AW817794.1	EST_HUMAN	Homo sapiens protein Kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
5973	26814	32478	1.47	2.0E-22	W39493.1	EST_HUMAN	PM1-ST0262-261169-001-d12 ST0262 Homo sapiens cDNA
6306	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	pc20601.L1 Scores_sarcomat_fibroblasts_NhlHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6904	22644	36529	1.78	2.0E-22	AL276522.1	EST_HUMAN	RC0-TN0079-150800-025-h12 TN0079 Homo sapiens cDNA
10001	23039	36630	0.85	2.0E-22	AA715315.1	EST_HUMAN	q76r06.x1 Scores_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER29 repetitive element;
10001	23039	36631	0.85	2.0E-22	AA715315.1	EST_HUMAN	mer29.13 MER29 repetitive element;
12058	25037	38745	1.52	2.0E-22	AW418980.1	EST_HUMAN	m04h11.s1 NCI_CGAP_P222 Homo sapiens cDNA clone IMAGE:1219269 3'
12139	25655	31954	2.33	2.0E-22	AL163280.2	NT	m04h11.s1 NCI_CGAP_P222 Homo sapiens cDNA clone IMAGE:1219269 3'
1827	16070	28175	2.05	1.0E-22	AW865517.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2874855 3'
2861	16774	28887	2.98	1.0E-22	U50871.1	NT	Homo sapiens chromosome 21 segment HS21C080
3497	18684	29876	1.53	1.0E-22	D14547.1	NT	PMA-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
7820	20971	34478	1.09	1.0E-22	BE084667.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10776	23809	37432	1.05	1.0E-22	AB365435.1	EST_HUMAN	Human DNA, SINE repetitive element
						EST_HUMAN	MRO-BT0689-220200-002-h07 BT0689 Homo sapiens cDNA
						EST_HUMAN	q208b07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020881 3' similar to contains MER29.b2
						EST_HUMAN	MER29 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23809	37433	1.05	1.0E-22	AI385435.1	EST_HUMAN	q208507.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29 b2
13078	26707		12.31	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element ;
3691	16824	26833	0.74	8.0E-23	AF168349.1	NT	IL2-JM0078-070400-061-F11 UM0078 Homo sapiens cDNA
3386	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
11233	24359	38000	3.74	7.0E-23	5031862	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
3520	16696		1.83	6.0E-23	AF168333.1	NT	Homo sapiens Not58 (D. melanogaster)-like protein (NOT58L) mRNA
4383	17826	30507	1.15	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12283	26211	32097	4.93	6.0E-23	AF224689.1	NT	Homo sapiens chromosome 21 segment HS21C049
12283	26211	32098	4.93	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12488	26335	32068	3.18	6.0E-23	AL209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
5560	18757	31788	4.01	5.0E-23	U82871.2	NT	q359c03.x1 Soares_besit_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
6369	26824	32898	3.69	5.0E-23	AF178818.1	NT	SW_MV10_MOUSE P23249 PROTEIN MOV-10 ;
7695	26824	32898	2.78	5.0E-23	AF178818.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
6670	16732	33110	0.87	3.0E-23	AL163227.2	NT	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin
6670	18732	33111	0.87	3.0E-23	AL163227.2	NT	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LL>
							Pongo pygmaeus difactory receptor (PPY116) gene, partial cds
8022	21105	34622	3.26	3.0E-23	AA130165.1	EST_HUMAN	Pongo pygmaeus difactory receptor (PPY116) gene, partial cds
9450	22566	36130	3.72	3.0E-23	Z70684.1	NT	Homo sapiens chromosome 21 segment HS21C027
9460	22566	36131	3.72	3.0E-23	Z70684.1	NT	Homo sapiens chromosome 21 segment HS21C027
10523	23559		1.42	3.0E-23	AW897827.1	EST_HUMAN	z335p09.1 Soares_pregnant_uterus_Nib-IPU Homo sapiens cDNA clone IMAGE:503668 5' similar to
							contains MER29.12 MER29 repetitive element ;
11372	24433		1.35	3.0E-23	AF280107.1	NT	Human endogenous retroviral element HC2
683	13888	26869	3.69	2.0E-23	AF280880.1	NT	Human endogenous retroviral element HC2
1168	16988		3.46	2.0E-23	M55270.1	NT	RC3-NIN0068-270400-011-h01 NN0068 Homo sapiens cDNA
2856	16970	29078	1	2.0E-23	P22105	SWISSPROT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
2856	16970	29080	1	2.0E-23	P22105	SWISSPROT	polypeptide 5 (CYP3A5) gene, partial cds
							Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
							Human matrix Gla protein (MGP) gene, complete cds
							TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
							TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3457	16824		1.11	2.0E-23	AI201458.1	EST_HUMAN	qs73f1.1x1 NCI_QGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
3810	16970		3.63	2.0E-23	BE165980.1	EST_HUMAN	MR3-HT0487-180200-113-g01 HT0487 Homo sapiens cDNA
4086	17240	30246	4.43	2.0E-23	H59831.1	EST_HUMAN	Y16402.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
4085	17240	30247	4.43	2.0E-23	H59831.1	EST_HUMAN	Y16402.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8057	21140		6.28	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
9044	22123	35685	0.85	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12266	26189		6.7	2.0E-23	M32658.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12844	26581		3.68	2.0E-23	AF009680.1	NT	Homo sapiens OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
12883	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4650	17786	30768	1.57	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4888	18018		5.42	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	801238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608833 5'
8551	21632	35189	4.61	1.0E-23	AA448097.1	EST_HUMAN	zr6208.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 PTR5 repetitive element;
10609	23992	37825	2.19	1.0E-23	BE409843.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37826	2.19	1.0E-23	BE409843.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
13082	26074	31654	1.35	1.0E-23	AW801816.1	EST_HUMAN	QV0-NN1020-170400-185-at11 NN1020 Homo sapiens cDNA
							ab75a08.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN.;
566	13758		1.67	9.0E-24	AA663213.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4771	17906	30888	1.12	8.0E-24	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4771	17906	30889	1.12	8.0E-24	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
6578	19740	33121	0.95	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.94	7.0E-24	AW637654.1	EST_HUMAN	QV0-DT0047-170200-122-ab08 DT0047 Homo sapiens cDNA
5281	18400		16.78	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 6'
10876	23991		1.61	7.0E-24	AW303317.1	EST_HUMAN	3x1703.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2819405 3' similar to contains AU repetitive element; contains MER19.12 MER19 repetitive element;
724	13906		2.21	6.0E-24	AB001421.1	NT	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4078	17234	30241	9.39	5.0E-24	AJ226043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7635	20985	34493	1.27	5.0E-24	AF223391.1	NT	

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17614		0.9	4.0E-24	BF369460.1	EST_HUMAN	RCO-GN0090-250900-022-H09 GN0090 Homo sapiens cDNA
6052	18234	32559	2.77	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.61 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK
8880	21659	35494	0.71	4.0E-24	AW813711.1	EST_HUMAN	P31786 POL POLYPROTEIN 1
11454	24514	38182	2.05	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-008 ST0197 Homo sapiens cDNA
12658	25448	32054	4.02	4.0E-24	AB028016.1	NT	801078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464468 5'
							Homo sapiens mRNA for KIAA1083 protein, partial cds
7228	20134	33551	0.73	3.0E-24	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJHS2>
7228	20134	33552	0.73	3.0E-24	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJHS2>
8818	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	h88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987850 3' similar to contains MER29.b2
8873	21763		1.24	3.0E-24	AW962076.1	EST_HUMAN	MER29 repetitive element
8885	22627	36198	3.79	3.0E-24	AL163262.2	NT	EST374149 IMAGE resequenced, MAGG Homo sapiens cDNA
12756	25501	32034	1.94	3.0E-24	BF127762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2422	15551	28678	2.55	2.0E-24	AA167539.1	EST_HUMAN	601810448F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053398 5'
3889	17058		0.82	2.0E-24	AW898189.1	EST_HUMAN	zp1109.r1 Stradiogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:600161 5'
7515	26219		0.83	2.0E-24	AL163209.2	NT	RC3-NIN0068-090500-021-003 NIN0068 Homo sapiens cDNA
7843	20712	34191	0.9	2.0E-24	AF086824.1	NT	Homo sapiens chromosome 21 segment HS21C009
7848	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rho3a-interacting citron kinase (Crik) mRNA, complete cds
8938	22017	35559	3.81	2.0E-24	AL119158.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone IMP12-6H13
8977	22055		0.9	2.0E-24	H69214.1	EST_HUMAN	DKFZp761L1712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
10068	23096	36698	1.06	2.0E-24	AJ621758.1	EST_HUMAN	Y82B09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
10058	23099	36699	1.06	2.0E-24	AJ521759.1	EST_HUMAN	MER28 repetitive element
12680	26153		21.43	2.0E-24	M28977.1	NT	677a09.x1 NCI_CGAP_K0411 Homo sapiens cDNA clone IMAGE:2138008 3'
1731	14881	27972	4.81	1.0E-24	7706340	NT	677a09.x1 NCI_CGAP_K0411 Homo sapiens cDNA clone IMAGE:2138008 3'
2738	15855		1.85	1.0E-24	AW820194.1	EST_HUMAN	Human O family dispersed repeat element
3085	16281	29278	0.72	1.0E-24	D88423.1	NT	Homo sapiens CG1-127 protein (LOC51646), mRNA
4385	17528		1.93	1.0E-24	AF143313.1	NT	QY0-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
							Mus musculus mRNA for HGT keratin, partial cds
							Homo sapiens PTEN (PTEN) gene, exon 2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	18085	33088	1.13	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C28 (Krt1-c28), mRNA
7720	20784	34272	4.85	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20959	34465	5.07	1.0E-24	BE144528.1	EST_HUMAN	MR0-HT0168-271189-005-408 HTD168 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901184.1	EST_HUMAN	CNM0-NN1010-190300-281-407 NN1010 Homo sapiens cDNA
11899	24984	38689	1.57	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA nes2e10.e1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
5111	18239	31208	2.7	7.0E-25	AA483944.1	EST_HUMAN	MER1 repetitive element; nc08a09.s1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
8413	21494	35025	3.7	7.0E-25	AA488846.1	EST_HUMAN	repetitive element; nt25f06.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
12003	24988	38683	3.64	7.0E-25	AA593540.1	EST_HUMAN	P38105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA;
7131	18557	34458	5.04	6.0E-25	W87623.1	EST_HUMAN	zh68h07.r1 Scores fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:416889 5'
7859	20561	34458	11.72	6.0E-25	7303390	NT	Mus musculus otogelin (Otog), mRNA
1683	14835	27620	1.61	5.0E-25	AW850271.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
11598	24949	38333	3.12	5.0E-25	AW978107.1	EST_HUMAN	EST1391217 IMAGE resequencing; MAGP Homo sapiens cDNA
1478	14831	27716	2.66	4.0E-25	T88107.1	EST_HUMAN	ye68h04.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121783 5'
3489	16555	27716	2.81	4.0E-25	AW887871.1	EST_HUMAN	FM3-OT0083-280200-001-g07 OT0083 Homo sapiens cDNA
4438	17576	36779	4.08	4.0E-25	BE170657.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
10144	23182	36779	0.83	4.0E-25	AA363873.1	EST_HUMAN	EST197917 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
2256	16389	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	RC3-BT0377-131288-031-F02 BT0377 Homo sapiens cDNA
3398	18368	29581	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3398	18368	29582	3.12	3.0E-25	P28622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	AL163210.2	NT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8532	21613	35149	5.42	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010 repetitive element; nt30h10.e1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.H1.L1
11287	24353	37893	2.7	3.0E-25	AA579013.1	EST_HUMAN	repetitive element;
1378	14533	27607	4.9	2.0E-25	5032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2382	15513	28841	7.33	2.0E-25	BE888016.1	EST_HUMAN	60151530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2893	15731	28848	3.71	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30436	1.81	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30437	1.81	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
8867	23006	38601	2.13	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides (SS) Homo sapiens cDNA
375	13583	28617	0.81	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434f10313_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1277	14434		2.07	1.0E-25	9835487	NT	Human endogenous retrovirus, complete genome

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4688	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-H10454-080100-002-H09 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8823788	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8823786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19855		0.95	1.0E-25	AA189080.1	EST_HUMAN	z445108.s1 Striatogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
6836	25838	33688	2.95	1.0E-25	AA582680.1	EST_HUMAN	nt54111.s1 NCL CGAP_K048 Homo sapiens cDNA clone IMAGE:1087749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	z88304.s1 Soares_fetal_heart_NbH-H16W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR6.t3 PTR5 repetitive element
9746	22810	36388	1.32	1.0E-25	X60680.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
9746	22810	36389	1.32	1.0E-25	X60680.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37620	3.11	1.0E-25	U69163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12280	25209	38384	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38385	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2553	15678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11262	24321		2.35	9.0E-26	AL905388.1	EST_HUMAN	QV-BT087-301298-006 BT087 Homo sapiens cDNA
12140	25901		6.33	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6811	18001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003328.1	NT	Homo sapiens X-linked antihydrolytic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4276	17420	30407	1.92	7.0E-26	AW340163.1	EST_HUMAN	nt02a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806366 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11986	24951		6.85	7.0E-26	AA115895.1	EST_HUMAN	zn30408.r1 Striatogene neuroepithelium NT2RAMI 837234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:MI4938 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	25596		5.49	7.0E-26	AW954559.1	EST_HUMAN	EST1366629 MAGE resequences, MAGC Homo sapiens cDNA
2300	16432	28565	3.83	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and hypoxanthine gene families
3427	16585	29611	0.69	6.0E-26	AA206131.1	EST_HUMAN	z452404.r1 Striatogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:945271 5'
10783	23786	37400	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10783	23786	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24984	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14386	27426	0.89	5.0E-26	AI706235.1	EST_HUMAN	aa38108.x1 Barslad aorta HFLR66 Homo sapiens cDNA clone IMAGE:2316519 3' similar to WP-F49C12.11 CE03371

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14368	27427	0.89	5.0E-26	AI708235.1	EST_HUMAN	ss38h108.x1 Barstead antia HPLR88 Homo sapiens cDNA clone IMAGE:2318519 3' similar to WP-F48C12.11 CE03371;
9612	22667		3.29	4.0E-26	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10897	23381	37813	2.84	4.0E-26	BE266187.1	EST_HUMAN	901191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3336210 5'
11604	24667	38342	1.38	4.0E-26	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1797	14946	28038	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2059	15200	28314	1.14	3.0E-26	AL049866.2	EST_HUMAN	DKFZp4341066_r1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp4341066 5'
2088	18228		3.34	3.0E-26	AA115896.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAM1 637234 Homo sapiens cDNA clone IMAGE:548943 5'
3878	17037	30035	1.41	3.0E-26	AA182484.1	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30035	1.41	3.0E-26	AA182484.1	EST_HUMAN	zo30f10.r1 Stratagene cdon (#637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3878	17037	30035	1.41	3.0E-26	AA182484.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
7051	20104	33621	6.08	3.0E-26	BF245458.1	EST_HUMAN	zo30f10.r1 Stratagene cdon (#637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11867	24855	38550	1.97	3.0E-26	AW875651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
11867	24855	38551	1.97	3.0E-26	AW875651.1	EST_HUMAN	601864683F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4083278 5'
11802	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
699	13882	26916	6.84	2.0E-26	AL163282.2	NT	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
1917	15060		3.07	2.0E-26	AL038039.2	EST_HUMAN	tn37d05.s1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1
3303	16477	29498	5.22	2.0E-26	X96994.1	NT	OFR repetitive element;
10691	24070		1.93	2.0E-26	D87876.1	NT	Homo sapiens chromosome 21 segment HS21C082
11493	24551	38228	2.98	2.0E-26	AI801412.1	EST_HUMAN	DKFZp668171_s1 586 (synonym: htss3) Homo sapiens cDNA clone DKFZp668171 3'
11704	24701		2.06	2.0E-26	AF055086.1	NT	Mutisculus mRNA for astrocytic phosphoprotein, PEA-15
12389	26276		1.76	2.0E-26	AB037866.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12604	26088	31656	2.33	2.0E-26		NT	ts88a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
139	13365	26398	8.96	1.0E-26	BE170371.1	EST_HUMAN	repetitive element; contains element MER20 MER20 repetitive element;
2105	16244	28365	1.42	1.0E-26	AL038039.2	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2751	15668		6.28	1.0E-26	AF281086.1	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
6980	20208		2.89	1.0E-26	BE165980.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
11131	24203		1.98	1.0E-26	AL038487.1	EST_HUMAN	QV4-H70538-020300-123-e02 HT0538 Homo sapiens cDNA
12855	26178		2.77	1.0E-26	H56093.1	EST_HUMAN	DKFZp43411910_r1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp43411910 5'
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (GADPH) mRNA, complete cds
							MRO-H70487-150200-113-g01 HT0487 Homo sapiens cDNA
							DKFZp668C2146_r1 586 (synonym: htss3) Homo sapiens cDNA clone DKFZp668C2146 5'
							CHFR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							UHFH-BMD-adv-4-10-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC8-FND138-110800-022-A02 FN0138 Homo sapiens cDNA
9603	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12143	25118		6.5	9.0E-27	BF445563.1	EST_HUMAN	ncat3c07.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:3253044 3' similar to contains OFR.t1 OFR repetitive element ;
11	13249	26249	4.22	8.0E-27	A831482.1	EST_HUMAN	W48-04.x1 NC1_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408160 3' similar to contains THR.b2 T-R repetitive element ;
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87708.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87708.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	15368	28409	1.82	8.0E-27	AW864776.1	EST_HUMAN	FM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
3254	16428	29448	1.8	8.0E-27	P12238	SWISSPROT	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 9) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16802	29821	0.76	8.0E-27	AF181887.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5812	19002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HITEBCB08 5'
7117	18543		2.85	8.0E-27	BE928560.1	EST_HUMAN	MR4-BT0398-250800-204-d08 BT0398 Homo sapiens cDNA
7192	20057	33467	2.49	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9410	22484	36048	1.63	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-083-d07 CT0315 Homo sapiens cDNA
9410	22484	36049	1.63	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-083-d07 CT0315 Homo sapiens cDNA
701	13884		1.77	7.0E-27	Z70684.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	H51H12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2876879 3' similar to TR:O76040
9058	22137		0.97	7.0E-27	D86984.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
10988	24067		3.7	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
10984	24045	37679	3.21	6.0E-27	M26897.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12004	25074	38781	1.55	6.0E-27	U63163.1	NT	Human nuclear protein (B23) mRNA, complete cds
7854	21004		0.73	5.0E-27	AL163303.2	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
10442	23477	37081	3.21	5.0E-27	BF668614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37082	3.21	5.0E-27	BF668614.1	EST_HUMAN	G02121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6883	20035	33444	1.65	4.0E-27	9810569	NT	G02121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Stap), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8126	21207		0.88	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8946	22884	36577	0.61	4.0E-27	AW890659.1	EST_HUMAN	QV0-OT0033-070300-152-510 OT0033 Homo sapiens cDNA
11903	24891	36592	2.62	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
2099	18239	28361	7.1	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4386	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-080100-001-411 BT0527 Homo sapiens cDNA
5462	18832	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862068 5'
42	13280	28266	9.28	2.0E-27	AF084187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1944	15087		24.24	2.0E-27	AA565345.1	EST_HUMAN	nt01b10.e1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000698 similar to gb:M17886 60S
3178	16353		13.94	2.0E-27	AW628172.1	EST_HUMAN	nt51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR-O76040
3296	16470	29489	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19867	33373	0.79	2.0E-27	H02855.1	EST_HUMAN	X36801.1 Soares placenta Nc2-F Homo sapiens cDNA clone IMAGE:150940 5' similar to
8282	21364	34853	1.17	2.0E-27	A1865347.1	EST_HUMAN	SP:HMGC_MOUSE_Q02591 HOMEBOX PROTEIN;
9489	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	nt28g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9895	23033	36625	0.83	2.0E-27	X80658.1	NT	nt08h05.e1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.L3 L1
10241	23276	36898	1.45	2.0E-27	M78590.1	EST_HUMAN	repetitive element;
10241	23276	36899	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
11197	24266	37801	3.91	2.0E-27	AU121685.1	EST_HUMAN	EST100738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBFCF07
11777	15087		6.43	2.0E-27	AA555345.1	EST_HUMAN	EST100738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBFCF07
12107	25087	38701	1.64	2.0E-27	AF218650.1	NT	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
449	13645		2.94	1.0E-27	AL163246.2	NT	nt01b10.e1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
1021	14192	27251	4.97	1.0E-27	AB028898.1	NT	ACD/C RIBOSOMAL PROTEIN P1 (HUMAN);
6874	18633	33222	6.51	1.0E-27	6005855	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33568	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
7010	20146	33567	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
8809	21886	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9188	22264		1.69	1.0E-27	BE079780.1	EST_HUMAN	RC8-BT0627-140200-011-E09 BT0627 Homo sapiens cDNA
9823	22863	38551	2.65	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24860	38694	3.05	1.0E-27	AF111083.1	NT	Bos taurus letraphilin 3 splice variant b2b1b mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	26567	2.17	9.0E-28	AU126280.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313;
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	AU126280 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12224	26173		3.04	9.0E-28	BF377869.1	EST_HUMAN	zp18g12.s1 Stratiotes fetal retina 837202 Homo sapiens cDNA clone IMAGE:609862 3'
12565	26003		13.39	6.0E-28	AW157571.1	EST_HUMAN	CN2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12565	26003		13.39	6.0E-28	AW157571.1	EST_HUMAN	eu83108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782011 3' similar to
12565	26003		13.39	6.0E-28	AW157571.1	EST_HUMAN	TR:Q06302 Q06302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
12565	26003		13.39	6.0E-28	AW157571.1	EST_HUMAN	AU142750 Y78A11 Homo sapiens cDNA clone Y78A11000824 5'
11463	24622	38182	1.65	7.0E-28	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12181	25141		5.04	7.0E-28	AV75348.1	EST_HUMAN	AV75348 CB Homo sapiens cDNA clone CBFACA12 5'
9119	22168		1.28	6.0E-28	AF016062.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	repetitive element contains element PTR5 repetitive element;
328	13542		2.75	5.0E-28	A1927003.1	EST_HUMAN	wt18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455892 3' similar to contains THR.b1
4116	17270	30269	38.94	5.0E-28	R79762.1	EST_HUMAN	THR repetitive element;
2689	15809	28828	1.46	4.0E-28	AW195063.1	EST_HUMAN	y88f10.f1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
3177	16362	28368	1.34	4.0E-28	BE409100.1	EST_HUMAN	pr83-09.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2885604 3' similar to SW:GG85_HUMAN
7483	20558	34030	3.56	4.0E-28	A198941.1	EST_HUMAN	Q08379 GOLGIN-96;
11105	24177		4.19	4.0E-28	AF028308.1	NT	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636305 5'
11255	24324		14.89	4.0E-28	AB038241.1	NT	qf68f10.x1 Scores testis NIH_T Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M18503 LINE-1
11278	20558	34030	4.34	4.0E-28	A198941.1	EST_HUMAN	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12822	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-f12 CT0254 Homo sapiens cDNA
12773	26068		1.62	4.0E-28	AW862350.1	EST_HUMAN	RC9-CT0379-070100-031-h01 CT0379 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1312	14468		2.29	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9027	22106	35647	2.28	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-09 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U53888.1	NT	Homo sapiens MHC class 1 region
12853	25433		3.77	3.0E-28	A831991.1	EST_HUMAN	w8807.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element
12803	25536		3.29	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0842-210200-013-03 BT0842 Homo sapiens cDNA
12865	25576	31993	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12866	25678	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
91	13328	26354	12.79	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	16671	28795	2.16	2.0E-28	A1348834.1	EST_HUMAN	qp35x06.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1010483 3' similar to contains L1.b2 L1 repetitive element
3446	16614	28632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	19604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	hw78cd03.x1 NCI_CGAP_JQM11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element
6460	19627		3	2.0E-28	BF212805.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.63	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary epimucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
11913	24900	38803	2.52	2.0E-28	AF224680.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424		1.74	2.0E-28	H06378.1	EST_HUMAN	y78cd09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1508	14661	27744	2.85	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2294	15423	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-603 BT0821 Homo sapiens cDNA
4691	17826		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8044	21127		1.95	1.0E-28	11426885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) [LOC803091], mRNA
8208	21290		3.03	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36089	4.75	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HOC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36720	5.91	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
10080	23118	36721	5.91	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12186	25145		7.68	1.0E-28	AA054182.1	EST_HUMAN	2f61cd01.r1 Soares retina N2b4f1R Homo sapiens cDNA clone IMAGE:380448 5'
13013	25681		4.58	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	26122	31643	1.8	9.0E-28	AW663987.1	EST_HUMAN	h17g06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878268 3'
12752	25498		2.57	8.0E-28	Q00130	SWISSPROT	HYPOTHETICAL GENE 60 PROTEIN
1632	14784	27870	1.98	7.0E-28	AW986447.1	EST_HUMAN	EST1376521 IMAGE resequences, MAGI Homo sapiens cDNA
13197	25779		9.08	7.0E-28	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	8.0E-28	A839748.1	EST_HUMAN	wp66b01.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12465	25342		6.19	6.0E-28	BE940438.1	EST_HUMAN	O15475 UNNAMED HERV.H PROTEIN ; contains LTR7 b1 LTR7 repetitive element ;
12587	25395		2.1	6.0E-28	BF568087.1	EST_HUMAN	RC3-UT0062-210800-021-c08 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-28	AL163203.2	NT	60218-082F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
8829	22008		8.35	5.0E-28	AW887641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12795	25531		1.49	5.0E-28	BE612448.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3304	16478		2.28	4.0E-28	AJ752367.1	EST_HUMAN	601451827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855728 5'
6133	19312		7.06	4.0E-28	BE184630.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8272	21354	34870	0.84	4.0E-28	AJ678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8272	21354	34871	0.84	4.0E-28	AJ678101.1	EST_HUMAN	wd35g08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2830170 3' similar to contains
8944	22023	35563	3.59	4.0E-28	J04988.1	NT	MER29.12 MER29 repetitive element ;
4536	17674	30868	1.31	3.0E-28	AB042287.1	NT	Human 90 kD heat shock protein gene, complete cds
4855	17968	30976	1.1	3.0E-28	BF383238.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoylhistidinol synthase, complete cds
6063	19235	32500	0.83	3.0E-28	BE314018.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
8831	22010	35548	3.23	3.0E-28	D38044.1	NT	601162857F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508627 5'
						NT	Human gene for Ah-receptor, exon 7-9
8500	22658	36119	1.22	3.0E-28	AW303317.1	EST_HUMAN	pxv1703.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813406 3' similar to contains Alu
9731	22798		1.49	3.0E-28	AL163248.2	NT	repetitive element contains MER19.12 MER19 repetitive element ;
10164	23201		0.61	3.0E-28	BE360127.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11546	24602	38278	2.26	3.0E-28	AA403053.1	EST_HUMAN	h03g01.x1 NC1 CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12385	25272		1.38	3.0E-28	D63882.1	NT	MER29 repetitive element ;
13092	26132		1.62	3.0E-28	D63882.1	NT	z662301.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726880 5' similar to TR:G1535789
505	13699	26727	0.98	2.0E-28	AF064868.1	NT	G1335769 GAG-POL POLYPROTEIN. ;
505	13699	26728	0.98	2.0E-28	AF064868.1	NT	Human HsLM15 mRNA for HsLM15, complete cds
						NT	Human HsLM15 mRNA for HsLM15, complete cds
						NT	Human HsLM15 mRNA for HsLM15, complete cds
						NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
						NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1563	14718	27794	7.8	2.0E-29	A1933604.1	EST_HUMAN	wr65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2482563 3' similar to TR:O15546 O15546
1563	14718	27795	7.8	2.0E-29	A1933604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	wr65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2482563 3' similar to TR:O15546 O15546
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	HERV-E ENVELOPE GLYCOPROTEIN;
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	H. sapiens mRNA for laminin-5, alpha3b chain
5946	19132	32446	0.78	2.0E-29	A1982459.1	EST_HUMAN	H. sapiens mRNA for laminin-5, alpha3b chain
6309	19481	32835	1.49	2.0E-29	A1908418.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
7732	19481	32835	1.28	2.0E-29	A1908418.1	EST_HUMAN	os71e04.x1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1
8164	21246	34768	1.16	2.0E-29	BE887157.1	EST_HUMAN	repetitive element;
8777	21856	35398	0.91	2.0E-29	10567821	NT	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355990 3' similar to contains element MER6 repetitive element;
8777	21856	35399	0.91	2.0E-29	10567821	NT	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355990 3' similar to contains element MER6 repetitive element;
9708	22757	36327	2.78	2.0E-29	AL163248.2	NT	601442200F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
9708	22757	36328	2.78	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11767	24760		1.97	2.0E-29	11426108	NT	Homo sapiens chromosome 21 segment HS21C048
8982	22071	35611	8.27	1.0E-29	AW983680.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
10850	23883	37503	2.81	1.0E-29	X80958.1	NT	Homo sapiens splicing factor similar to chn1 (SPF31), mRNA
6712	19870	33261	3.53	9.0E-30	AA781215.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
12268	28200		4.55	9.0E-30	11422746	NT	R.tattus RYA9 mRNA for a potential ligand-binding protein
6449	19616		10.5	8.0E-30	F08888.1	EST_HUMAN	re20e07.e1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1
8465	21546	35078	2.26	8.0E-30	AA388873.1	EST_HUMAN	MER4 repetitive element;
8882	21981	35495	2.79	8.0E-30	AI597072.1	EST_HUMAN	Homo sapiens zinc/ferron regulated transporter-like (ZIRT), mRNA
1646	14697		1.07	7.0E-30	BE091133.1	EST_HUMAN	HS23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05
1814	14963	28056	1.57	6.0E-30	D26303.1	NT	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
3268	16433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
4881	16433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF177271.1	NT	Human mRNA for integrin alpha subunit, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17276	30274	43.22	5.0E-30	A1309992.1	EST_HUMAN	1092003.x1 NCL_CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element.
5353	25928		5.79	5.0E-30	U87931.1	NT	Human acetylcholinesterase (ACOE2) gene, exon 7
11128	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.78	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	18344	28470	2.38	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2210	18344	28471	2.38	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
9106	22185	35728	1.55	4.0E-30	AW812488.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	A1338551.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
3853	17013	30013	1.15	3.0E-30	AF128893.1	NT	contains MER29 b2 MER29 repetitive element;
8138	21220		0.53	3.0E-30	AF078178.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
8883	21703		0.45	3.0E-30	AF078178.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10849	23683	37284	0.74	3.0E-30	BE350127.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11482	24541	38211	1.52	3.0E-30	P34056	SWISSPROT	h109301.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3
892	13876	26808	1.42	2.0E-30	AW857315.1	EST_HUMAN	MER29 repetitive element.
1108	14273		2.53	2.0E-30	P08688.1	EST_HUMAN	TRANSCRIPTION FACTOR AP-2
1509	14662	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	GM0-CT0307-310100-168-h03 CT0307 Homo sapiens cDNA
2779	15895	29005	9.83	2.0E-30	BE765232.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA
2986	16162	29179	6.83	2.0E-30	AF114156.1	NT	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
3889	17048	30048	1.95	2.0E-30	AW206881.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
4900	18030	31018	2.02	2.0E-30	BE288945.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
4900	18030	31019	2.02	2.0E-30	BE288945.1	EST_HUMAN	UIH-B11-efo-c-12-0-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722668 3'
6734	21814	35349	4.89	2.0E-30	C18839.1	EST_HUMAN	601119880F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
8896	21615	35452	1.71	2.0E-30	BE670617.1	EST_HUMAN	601119880F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
8836	21615	35453	1.71	2.0E-30	BE670617.1	EST_HUMAN	C18839 Human placenta cDNA (TFIIJwara) Homo sapiens cDNA clone GEN-670C01 5'
10201	23238	36828	3.78	2.0E-30	AW971588.1	EST_HUMAN	7687c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN
							P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
							7687c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN
							P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
							EST383557 IMAGE resequences, MAGL Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	23322	36824	6.31	2.0E-30	AW470791.1	EST_HUMAN	h833d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875469 3' similar to contains THIR.b3
287	13514	26548	10.87	1.0E-30	C18939.1	EST_HUMAN	THIR repetitive element; C18939 Human placenta cDNA (TF-ijivara) Homo sapiens cDNA clone GEN:570C01 5'
561	13744	26760	1.62	1.0E-30	AW468997.1	EST_HUMAN	h830b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810691 3' similar to contains MER1.13 MER1 MER1 repetitive element;
734	13918	28958	5.15	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2786	15418	28550	11.56	1.0E-30	AA694377.1	EST_HUMAN	ac77b08.x1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:868589 3'
2633	16658	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	602022660F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157991 5'
3120	16296	29310	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST188988 HCC cell line (matelastis to liver in mouse) II Homo sapiens cDNA 5' end
7901	20953	34460	1.96	1.0E-30	BF183230.1	EST_HUMAN	601806832F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
8176	21258	34780	0.49	1.0E-30	BE081586.1	EST_HUMAN	MRO-BT0249-081269-101-g01 BT0249 Homo sapiens cDNA
12788	26117		1.57	1.0E-30	AA289211.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
12937	26025		5.31	1.0E-30	H55583.1	EST_HUMAN	CHR220632 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3882	17022	30020	0.8	9.0E-31	IT73025.1	EST_HUMAN	yc65e06.r1 Stratiogene liver (#837224) Homo sapiens cDNA clone IMAGE:86570 5'
3882	17022	30021	0.8	9.0E-31	IT73025.1	EST_HUMAN	yc65e06.r1 Stratiogene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
8519	21600	35135	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88b08.r1 Scores infant brain 1N18 Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:U12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8519	21600	35136	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88b08.r1 Scores infant brain 1N18 Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:U12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8825	21904		1.89	9.0E-31	Z38283.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05F03 3'
8827	21606	35445	0.55	9.0E-31	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
13183	25776	31634	1.29	9.0E-31		NT	Mus musculus syndecan 4 (Sdc4), mRNA
1102	14267	27325	2.52	8.0E-31		NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2484	15611		7.83	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
729	13911		1.69	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2733	15950	28982	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Ju24 Homo sapiens cDNA clone IMAGE:3182012 3'
2733	15950	28983	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Ju24 Homo sapiens cDNA clone IMAGE:3182012 3'
8595	21676	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8595	21676	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9466	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	601904125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
						NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3769	16930		3.42	6.0E-31	AF229391.1	NT	
8347	21428		1.39	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8526	21607	35148	0.76	6.0E-31	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10976	24065	37089	1.43	6.0E-31	AU119105.1	EST_HUMAN	MER28 repetitive element ;
12327	25236	32108	3.7	6.0E-31	AW372893.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12459	26947		2.54	6.0E-31	BE884488.1	EST_HUMAN	RG5-BT0377-081289-031-D12 BT0377 Homo sapiens cDNA
197	13420	28460	3.39	5.0E-31	M60694.1	NT	601433097F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	28451	3.39	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
809	13798		3.02	4.0E-31	AJ271735.1	NT	7068704.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	SIMILAR TO POGO ELEMENT ; contains L1.H L1 repetitive element ;
1861	15007		2.09	4.0E-31	AL163280.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2949	16963		1.57	4.0E-31	5730038	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
10764	23787	37402	0.46	4.0E-31	AF084464.1	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
12787	25526		1.55	4.0E-31	11430273	NT	ACETYL GALACTOSAMINYL TRANSFERASE (GALNAC-T1)
12924	26509		2	4.0E-31	AB008681.1	NT	Homo sapiens chromosome 21 segment HS21C080
2660	15782	28867	1.75	3.0E-31	6005871	NT	Homo sapiens SET domain and maltrin transposase fusion gene (SETIMAR) mRNA
7494	20569	34041	8.04	3.0E-31	4825853	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7663	20730	34206	1.23	3.0E-31	11420329	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
8355	21436		1.51	3.0E-31	AL163208.2	NT	Homo sapiens gene for activin receptor type IIB, complete cds
9179	22819	36397	2.59	3.0E-31	D14523.1	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
10822	23855	37477	0.86	3.0E-31	AA421242.1	EST_HUMAN	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (18kD, ASH1) (NDUFB8) mRNA
10867	23862	37682	2.03	3.0E-31	P11174	SWISSPROT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
11421	24482		3.47	3.0E-31	BF056327.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
1907	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	Horse mRNA for ferritin L-chain, complete cds
2288	15420	28552	1.05	2.0E-31	AJ393388.1	EST_HUMAN	z066404.t1 Scores_NHT Homo sapiens cDNA clone IMAGE:731047 5'
2416	15545	28874	2.22	2.0E-31	AL119245.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
2511	15637	28758	4.63	2.0E-31	AA458824.1	EST_HUMAN	601458531F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3862088 5'
5389	18591	31563	0.76	2.0E-31	AW444463.1	EST_HUMAN	QV2.LT0051-260300-111-403 LT0051 Homo sapiens cDNA
							tp44g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
							DKFZp761G1513 t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
							aa88711.s1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
							THR12 THR repetitive element ;
							U1H-B18-abb-f09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	h08901.x1 NCL CGAP_Ku13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.B3
9277	22363						MER29 repetitive element;
9408	22482		1.53	2.0E-31	AA877784.1	EST_HUMAN	h08904.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1191055 3' similar to TR-Q13537 Q13537
10110	23146	36046	3.46	2.0E-31	7691536	NT	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
10280	23315	36914	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10280	23315	36915	2.75	2.0E-31	BE408611.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
12430	26305		2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12578	26202		3.49	2.0E-31	AF148512.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
17	13255		2.59	2.0E-31	AI114627.1	EST_HUMAN	Homo sapiens hexokinase II gene, promoter region
1698	14948	26256	9.91	1.0E-31	UB3153.1	NT	HA1110 Human fetal liver cDNA library/Homo sapiens cDNA
1698	14948	27832	2.68	1.0E-31	O95371	SWISSPROT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
1698	14948	27833	2.68	1.0E-31	O95371	SWISSPROT	(MAGE-B1) genes, complete cds
1698	14948	27834	2.68	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
6407	18609	31581	3.97	1.0E-31	AW391679.1	EST_HUMAN	OLFACTORY RECEPTOR 2C1
6281	19435	32781	2.57	1.0E-31	AF049727.1	NT	MER3-ST0220-151269-028-408_1 ST0220 Homo sapiens cDNA
7441	20518	33990	0.94	1.0E-31	AF126145.1	NT	Homo sapiens mitochondrion fatty acid CoA ligase form XL-III mRNA, nuclear mRNA encoding
8005	21055	34587	1.35	1.0E-31	BE972818.1	EST_HUMAN	Bos taurus xenobiotic/medium-chain fatty acid CoA ligase form XL-III mRNA, nuclear mRNA encoding
10441	23476	37080	0.5	1.0E-31	UB3153.1	NT	mitochondrial protein, complete cds
11158	24227	37857	2.35	1.0E-31	AI086434.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835293 5'
6778	19931	33327	2.19	9.0E-32	AV723978.1	EST_HUMAN	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
7530	20803	34077	0.88	9.0E-32	L31770.1	NT	(MAGE-B1) genes, complete cds
7766	20825		0.91	9.0E-32	11430822	NT	q271h03.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR-Q16595
2139	15275	26397	5.1	8.0E-32	AI056770.1	EST_HUMAN	Q16595 FRATAXIN.;
5599	18794	31843	0.77	8.0E-32	AW087214.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAAG01 5'
12406	25285		2.98	7.0E-32	X17283.1	NT	Bos taurus vacuolar H ⁺ -ATPase subunit mRNA, complete cds
7523	20568		1.32	6.0E-32	BE888016.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
							car15a09.x1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
							RC2-BN0048-200300-015-604 BN0048 Homo sapiens cDNA
							Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphan and neighbouring non-amplified region
							601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12868	26181		2.5	6.0E-32	AA864653.1	EST_HUMAN	oh37c03.s1 NCL_CGAP_K048 Homo sapiens cDNA clone IMAGE:1458972 3' similar to contains L1.13 L1 repetitive element:
1059	14225	27282	10.42	6.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
854	14127		1.84	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G046
7779	20835	34326	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-H05 BT0311 Homo sapiens cDNA
468	13693	26699	2.84	3.0E-32	Y17283.1	NT	Homo sapiens FL-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
2973	16149	29168	0.75	3.0E-32	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
8584	22849	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
8584	22849	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
11166	24237	37638	3.43	3.0E-32	AA777621.1	EST_HUMAN	z656d07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element:
12433	25307		7.95	3.0E-32	BE278086.1	EST_HUMAN	G01156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29168	4.95	3.0E-32	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
13020	26671		6.47	3.0E-32	BE278086.1	EST_HUMAN	G01156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32807	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6808	19768	33156	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6608	19768	33157	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8473	21554	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	z666c08.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21554	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	z666c08.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16338		1.25	1.0E-32	BE743289.1	EST_HUMAN	G01573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:383439 5'
7200	20065	33476	6.64	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8795	21874	35413	4.58	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element:

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539
6550	18712		3.17	9.0E-33	AF223391.1	NT	WW DOMAIN BINDING PROTEIN 11.1
8988	22067	35607	1.81	9.0E-33	BF347220.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11038	24117		4.55	9.0E-33	AL163280.2	NT	802021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15982	28491	3.04	7.0E-33	AI690115.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2714	15932		7.95	7.0E-33	AV730056.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
3314	16487		15	7.0E-33	AW971907.1	EST_HUMAN	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
9147	22228		0.87	7.0E-33	X54890.1	NT	AV730056 HTF Homo sapiens cDNA clone HTFAVE08 5'
11067	24142	37777	1.88	7.0E-33	BF347228.1	EST_HUMAN	EST383308 MAGE resequences, MAGL Homo sapiens cDNA
11526	24882	38268	1.59	7.0E-33	AW971908.1	EST_HUMAN	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
12413	26282	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
3830	18990		0.93	6.0E-33	AL163285.2	NT	EST383357 MAGE resequences, MAGL Homo sapiens cDNA
6192	19368	32717	0.91	6.0E-33	F30631.1	EST_HUMAN	no16h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L.1.H L.1 repetitive element;
6192	19368	32718	0.91	6.0E-33	F30631.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
8778	21657	35400	1.86	6.0E-33	J04038.1	NT	HSPD21201 HM3 Homo sapiens cDNA clone e4000107H06
8899	21678	35517	3.12	6.0E-33	11429186	NT	HSPD21201 HM3 Homo sapiens cDNA clone e4000107H08
10214	23250	36839	2.03	6.0E-33	6755909	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
10214	23250	36840	2.03	6.0E-33	6755909	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC83277), mRNA
1818	14987		1.9	5.0E-33	BF379515.1	EST_HUMAN	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1931	15074		1.32	5.0E-33	11141884	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1947	15090	28180	1.63	5.0E-33	4507208	NT	QV1-FTD169-100700-271-02 FT0169 Homo sapiens cDNA
1947	15090	28181	1.63	5.0E-33	4507208	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC6A7), mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens spermidine synthase (SRM) mRNA
4169	17319	30312	0.66	5.0E-33	AB014599.1	NT	Homo sapiens spermidine synthase (SRM) mRNA
10454	23489	37087	0.82	5.0E-33	AW264678.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C086
10454	23489	37088	0.82	5.0E-33	AW264678.1	EST_HUMAN	Homo sapiens mRNA for KIAA0699 protein, partial cds
							xq33f11.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
							xq33f11.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	26185		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1162	14316		2.25	4.0E-33	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15029	28454	3.37	4.0E-33	4768987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1), mRNA
2491	15618		1.16	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2810	15734	28860	4.78	4.0E-33	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4806	17743	30722	2.38	4.0E-33	AW283349.1	EST_HUMAN	UIH-B12-shl-c-03-Q-ULs1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA063053.1	EST_HUMAN	271a08.1 Stratagene colon (937204) Homo sapiens cDNA clone IMAGE:510038 6' similar to gb:X12671_mat HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	19687	33060	0.79	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	19687	33061	0.78	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.62	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element;
1114	14278		5.83	3.0E-33	BE350127.1	EST_HUMAN	MER28 repetitive element;
2522	18064		1.16	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCFCF09 3'
10655	23689	37298	0.87	3.0E-33	AA861610.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR-Q13679 Q13579 MARINER TRANSPOSASE;
18	13256		1.57	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_Nb-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.H1 OFR repetitive element;
107	13256		5.53	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_Nb-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.H1 OFR repetitive element;
4639	17677		4.53	2.0E-33	BE180039.1	EST_HUMAN	MFR0-HT0405-160300-202-008 HT0405 Homo sapiens cDNA
5100	18228	31189	8.64	2.0E-33	AA626693.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:U00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31294	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6553	19715	33091	1.39	2.0E-33	AI27492.1	EST_HUMAN	q08401.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1680161 3'
9301	22377		2.15	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver spleen_1NFL3_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13247		1.81	1.0E-33	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7565	20637	34113	0.86	1.0E-33	MI13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10227	26229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24655	38340	1.56	1.0E-33	AW98818.1	EST_HUMAN	QV3-BN0047-230200-102-003 BN0047 Homo sapiens cDNA
11982	24647	38662	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW904491.1	EST_HUMAN	RC5-NN1055-280400-021-G03 NN1055 Homo sapiens cDNA
12829	13247		5.7	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12960	25636	31979	2.19	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
13179	25766		4.77	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2240	16373	28501	0.98	8.0E-34	8822751	NT	Homo sapiens hypothetical protein FLJ108001 (FLJ10800), mRNA
4620	17157	30739	1.93	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT0258-071298-019-g07 BT0258 Homo sapiens cDNA
7874	21024	34537	0.97	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0359-200100-001-003 BT0359 Homo sapiens cDNA
1478	14629	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	Yd16c05.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:108320 5'
10204	14629	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	Yd16c05.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:108320 5'
12482	25334		3.85	7.0E-34	H12886.1	EST_HUMAN	X14c10.1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	28711	1.74	6.0E-34	U10691.1	NT	Human G2 protein mRNA, partial cds
483	13677	28712	1.74	6.0E-34	U10691.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.58	6.0E-34	AW98811.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12280	25215	32099	2.22	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hac-1) gene
1929	15072		3.15	5.0E-34	T706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	18295	31257	5.24	6.0E-34	U30683.1	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
9067	22146	35683	1.17	5.0E-34	AF078779.1	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
10890	23974	37805	2.02	5.0E-34	AB037850.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11532	24588		1.93	5.0E-34	AL163209.2	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
2054	15195	28309	2.09	4.0E-34	AJ804687.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G009
3241	18415	29430	0.9	4.0E-34	5803168	NT	Homo sapiens chromosome 21 segment HS21G009
5981	18168	32488	0.82	4.0E-34	AA881773.1	EST_HUMAN	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
9238	22315	35657	0.83	4.0E-34	BF208778.1	EST_HUMAN	af35c01.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1407836 3'
6361	18531	32880	0.86	3.0E-34	M37277.1	NT	601874950F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102213 5'
11420	24481		2.96	3.0E-34	BF035327.1	EST_HUMAN	Human Ig gamma H-chain D-region genes, partial cds
9152	22230	35774	0.75	2.0E-34	AJ878101.1	EST_HUMAN	601458531F1 NIH_MGC 98 Homo sapiens cDNA clone IMAGE:3962088 5'
9152	22230	35775	0.75	2.0E-34	AJ878101.1	EST_HUMAN	MER28.12 MER29 repetitive element;
11431	24492	38156	8.54	2.0E-34	P51805	SWISSPROT	w35g06.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER28.12 MER29 repetitive element;
							PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11431	24492	38157	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1634	14687	27767	10.13	1.0E-34	P12238	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14867		7.18	1.0E-34	AU136824.1	EST_HUMAN	AU136824 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
3764	16825	29827	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anthrillio ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4802	17739		8.28	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0505-240400-016-h08 BT0505 Homo sapiens cDNA
6266	19440	32787	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886899 5'
6266	19440	32788	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886899 5'
8527	22592	38163	0.64	1.0E-34	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9898	22638	38523	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1569_r1 584 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564A1569 5'
11469	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470562F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11469	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470562F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11436599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12680	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.at NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:U68203
12680	26680		5.84	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3735	16836	29900	1.3	9.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
232	13453		7.21	8.0E-35	6031190	NT	H17706.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2868787 5'
1776	14925	28019	3.63	8.0E-35	BF589837.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1776	14925	28020	3.63	8.0E-35	BF589837.1	EST_HUMAN	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4889	18118	31087	2.61	8.0E-35	BF183195.1	EST_HUMAN	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
10829	24011	37945	1.53	8.0E-35	BE378480.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
12404	25283		5.89	8.0E-35	BF569282.1	EST_HUMAN	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
6613	19773	33184	1.51	7.0E-35	11425417	NT	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1445	14598	27875	1.08	8.0E-35	AA757115.1	EST_HUMAN	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
2025	15168	28271	4.63	6.0E-35	6005975	NT	O75912 DIACYLGLYCEROL KINASE IOTA ;
4184	17314	30309	0.8	6.0E-35	AW297161.1	EST_HUMAN	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
8081	21163	34880	4.03	6.0E-35	6005921	NT	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
8906	21885	35524	0.57	6.0E-35	X94232.1	NT	ncs3408.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8806	21985	35525	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
9867	22307	38492	0.61	6.0E-35	AB002394.1	NT	Human mRNA for KIAA0368 gene, partial cds
10107	23145	36743	2.97	6.0E-35	AB037988.1	NT	Human sapiens mRNA for KIAA1365 protein, partial cds
148	13373	28408	0.61	5.0E-35	AF164830.1	NT	Human sapiens carboxyl phosphatase synthetase 1 mRNA, complete cds
1746	14895	27869	2.25	5.0E-35	X63382.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2844	16558	23067	0.99	5.0E-35	AB007866.2	NT	Human sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	28271	2.87	5.0E-35	6812639	NT	Human sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17667	30653	1.72	5.0E-35	AF023288.1	NT	Human sapiens cdc2 kinase (CLK2), protein1, cdc21, glucocorticoidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoidase pseudogenes; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE890992.1	EST_HUMAN	601431084F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21488	35015	2.17	5.0E-35	AI208765.1	EST_HUMAN	q336c05.x1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q82539 HYPOTHETICAL PROTEIN KIAA0248. ;
8405	21488	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	q336c05.x1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q82539 HYPOTHETICAL PROTEIN KIAA0248. ;
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	2H84F12.J1 Soares_fetal_liver_spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-36	BE257607.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1882	15008	28114	11.21	4.0E-35	H01193.1	EST_HUMAN	y188a07.f1 Soares_fetal_liver_spleen INFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element. ;
7358	20437		1.67	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.B3 MER29 repetitive element. ;
8715	21795	35332	8.05	4.0E-35	AL046593.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L148 5'
12098	25078	38786	2.5	4.0E-35	AF114150.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
1610	14763	27843	93.92	3.0E-35	BE288182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2408	15539		2.64	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	7r25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566381 3' similar to TR:Q9QZH7
5458	18656	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	Q9QZH7 F-BOX PROTEIN FBL2. ;
9889	22738		1.45	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10378	23413	37022	1.5	3.0E-35	AW003083.1	EST_HUMAN	vr03a05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480482 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE. ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-35	N88865.1	EST_HUMAN	K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6832 5' similar to
1215	14376	27436	1.89	2.0E-35	T11903.1	EST_HUMAN	REPEITIVE ELEMENT
2292	15424	28558	4.56	2.0E-35	AB018413.1	NT	A971F Heart Homo sapiens cDNA clone A971
2748	16865	28976	1.13	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3388	16556	28670	1.08	2.0E-35	6912459	NT	h88a12.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to
3386	16556	28671	1.08	2.0E-35	6912459	NT	SW:TR12 HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3847	16810		0.77	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0671), mRNA
4019	17176	30184	0.85	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17176	30185	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
4792	17827		3.01	2.0E-35	H48239.1	EST_HUMAN	cDNA clone TCBAP4328
5700	18804	32186	1.83	2.0E-35	BF332417.1	EST_HUMAN	V19a12.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
7263	20336	33785	0.8	2.0E-35	BE832636.1	EST_HUMAN	QV0-BT0701-210400-169-B04 BT0701 Homo sapiens cDNA
7253	20336	33786	0.8	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11036	24115	37749	2.93	2.0E-35	X69417.1	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12157	16556	28570	1.22	2.0E-35	6912459	NT	H. sapiens PROS-27 mRNA
12342	26247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	26247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12831	25614		7.22	2.0E-35	AL163210.2	NT	601469774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
13056	16005	26372	1.74	2.0E-35	N88865.1	EST_HUMAN	601469774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
47	13286	26285	5.78	1.0E-36	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
47	13286	26296	5.78	1.0E-35	AA631949.1	EST_HUMAN	K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6832 5' similar to
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	REPEITIVE ELEMENT
771	13952	27001	35.82	1.0E-36	AW389473.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
932	14107		1.28	1.0E-35	T87947.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
2607	15730	28847	1.89	1.0E-35	7705994	NT	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
2628	15940	28050	1.34	1.0E-35	BE350127.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
							IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
							Yd83a01.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
							SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
							Homo sapiens hypothetical protein (LOC51233), mRNA
							h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28.b3
							MER28 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2828	15040	23051	1.34	1.0E-36	BE350127.1	EST_HUMAN	h106g01.x1 NCI_CGAP_K6413 Homo sapiens cDNA clone IMAGE:3148286 3' similar to contains MER29.b3
3212	16388	28387	1.87	1.0E-35	6006030	NT	MER29 repetitive element;
3232	16403	28418	1.87	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TC6B1L) mRNA
3232	16403	28418	1.87	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
4542	17680	30661	4.82	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
4542	17680	30662	4.82	1.0E-35	7658905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5627	18821	31896	1.48	1.0E-35	7658905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
7135	18561	31475	0.74	1.0E-35	11528236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7135	18561	31475	0.74	1.0E-35	AW608665.1	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7652	20720	34198	0.99	1.0E-35	AW608665.1	EST_HUMAN	MR1-ST0111-111193-011-407 ST0111 Homo sapiens cDNA
7819	20874	34373	0.91	1.0E-35	AB033105.1	NT	MR1-ST0111-111193-011-407 ST0111 Homo sapiens cDNA
9742	26861	36383	2.46	1.0E-35	11418002	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
9742	25861	36394	2.46	1.0E-35	AL1158595.1	EST_HUMAN	Homo sapiens KIAA0846 gene product (KIAA0846), mRNA
10805	23838	37482	0.72	1.0E-35	BF589594.1	EST_HUMAN	AUT58595 PLACES Homo sapiens cDNA clone PLACES3000382 3'
10805	23838	37483	0.72	1.0E-35	BF589594.1	EST_HUMAN	AUT58595 PLACES Homo sapiens cDNA clone PLACES3000382 3'
12055	25036	38743	1.49	1.0E-35	AB028980.1	NT	hna06d08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR-O31341
12055	25036	38744	1.49	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE ;
12062	25043		2.04	1.0E-35	AI625119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12405	25284		1.26	1.0E-35	11418110	NT	hna06d08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR-O31341
12808	26539		2.49	1.0E-35	BE782832.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ;
6131	19310	32850	0.67	8.0E-36	X78479.1	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
9430	22804	36070	0.76	8.0E-36	AA348480.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
2897	16173	29182	1.53	7.0E-36	AW657578.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
3188	16363		5.25	7.0E-36	4957468	NT	B. bovis BBSv mRNA for schistatin
6273	18492	31360	1.09	7.0E-36	Q27409	SWISSPROT	EST54838 Hippocampus II Homo sapiens cDNA 5' and similar to similar to endogenous retrovirus 9, 5' LTR
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	GM1-CT0315-091289-083-d07 CT0315 Homo sapiens cDNA
7832	20887	34389	6.31	7.0E-36	U06872.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7832	20887	34390	6.31	7.0E-36	U06872.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
12570	25388	32040	27.38	7.0E-36	AF062051.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2060	16201	28515	1.92	6.0E-36	7708822	NT	Homo sapiens <i>hijurin 2 (NINL2)</i> , mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens <i>TCL6</i> gene, exon 12
3729	16890	29894	0.59	6.0E-36	BF515101.1	EST_HUMAN	UHL-BW1-ant-c-12-UJI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
6446	18646	31624	7.17	6.0E-36	AI435160.1	EST_HUMAN	HS3K003.X1 Soares_NSF_F8_9W_OT_PA.P_91 Homo sapiens cDNA clone IMAGE:2128195 3' similar to HS3K003.X1 Soares_PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33782	3.03	6.0E-36	AW780143.1	EST_HUMAN	hs06M02.X1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT;
8863	21932	36471	4.62	6.0E-36	AF208161.1	NT	Homo sapiens <i>syncytin precursor</i> , mRNA, complete cds
10490	23465		0.63	6.0E-36	C16927.1	EST_HUMAN	G16927 Clontech human <i>aria polyA+</i> mRNA (#6572) Homo sapiens cDNA clone GEN:535C11 5'
11841	24830	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	HS3K009.X1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER8.b2 MER9 repetitive element;
140	13366	26399	15.16	6.0E-36	AL271735.1	NT	Homo sapiens <i>Xq pseudautosomal region</i> ; segment 1/2
2809	18923	29033	21.08	5.0E-36	BE388496.1	EST_HUMAN	601285557F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3700	16861	29863	3.24	5.0E-36	AL163208.2	NT	Homo sapiens <i>chironosome 21 segment HS21C009</i>
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens <i>API5-like 1 (API5L1)</i> , mRNA
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens <i>API5-like 1 (API5L1)</i> , mRNA
7866	21016	34528	0.69	6.0E-36	11078227	NT	Homo sapiens <i>N-ethylmaleimide-sensitive factor (NSF)</i> , mRNA
12155	13366	26399	6.11	5.0E-36	AL271735.1	NT	Homo sapiens <i>Xq pseudautosomal region</i> ; segment 1/2
12459	26322	32095	2.36	5.0E-36	11417882	NT	Homo sapiens <i>calcineurin binding protein 1 (KIAA0330)</i> , mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	PM8-BN0178-100400-001-g04 BN0178 Homo sapiens cDNA
1677	14829	27613	1.36	4.0E-36	BE382574.1	EST_HUMAN	601286574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2297	15428		4.14	4.0E-36	AW247772.1	EST_HUMAN	2820020.Sprtime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3435	16603	29622	1.1	4.0E-36	BE369289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3435	16603	29623	1.1	4.0E-36	BE388298.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4977	18008	30962	0.69	4.0E-36	AL163204.2	NT	Homo sapiens <i>chironosome 21 segment HS21C004</i>
5833	18024		0.66	4.0E-36	RG4023.1	EST_HUMAN	Y19705.1 Soares placenta Nk2-IP Homo sapiens cDNA clone IMAGE:139713 5'
6180	18066	32704	2.49	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7831	20688	34398	1.78	4.0E-36	M33320.1	NT	Human platelet <i>Glycoprotein IIb (GP1Ib) gene</i> , exons 2-29
8762	21831	35369	1.45	4.0E-36	D87676.1	NT	Homo sapiens <i>DNA for amyloid precursor protein</i> , complete cds
8762	21831	35370	1.45	4.0E-36	D87676.1	NT	Homo sapiens <i>DNA for amyloid precursor protein</i> , complete cds
11235	24304	37941	3.13	4.0E-36	AA400370.1	EST_HUMAN	zu68c10.J1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12476	25928		1.91	4.0E-36	11420518	NT	Homo sapiens <i>nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2)</i> , mRNA
12520	25961		4.27	4.0E-36	AV763628.1	EST_HUMAN	AV763628 TP Homo sapiens cDNA clone TPGBH01 5'
714	13898	26934	2.83	3.0E-36	AF098810.1	NT	Homo sapiens <i>neurexin III-alpha</i> gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7682401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jpl-pending), mRNA
11368	24429	38088	1.84	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW980378.1	EST_HUMAN	QV0-OT0030-240300-174-M4 OT0030 Homo sapiens cDNA
5603	18798	31848	2.68	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
5970	19156	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bonto Scores Homo sapiens cDNA clone HIBB128 5' end
6706	19884	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	yc44407.1 Stratagene liver (4837224) Homo sapiens cDNA clone IMAGE:83508 5'
9688	22643	36212	0.94	2.0E-36	BF512794.1	EST_HUMAN	UJ-H-BW1-emu-e-11-0-UJ.e1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE148523.1	EST_HUMAN	RC1-H-T0217-131189-021-h07 HT0217 Homo sapiens cDNA
2212	15346	28476	1.71	1.0E-36	BE148523.1	EST_HUMAN	RC1-H-T0217-131189-021-h07 HT0217 Homo sapiens cDNA
2275	15408	28538	1.83	1.0E-36	BF079761.1	EST_HUMAN	602198403F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3425	16594	32344	3.33	1.0E-36	AF156962.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5847	19037	32344	0.64	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022.1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AB67714.1	EST_HUMAN	vb37c12.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6519	19884	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	yg38g10.1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;
6519	19884	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	yg38g10.1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;
6820	19873	33361	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229.1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21228	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	z051a12.1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z051a12.1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.78	1.0E-36	AA420467.1	EST_HUMAN	nc60a08.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60a08.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone IMAGE:34529 5'
8373	21454	34978	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9229	22307	35850	3.33	1.0E-36	AW103688.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10320	23355	36984	3.83	1.0E-36	BF384189.1	EST_HUMAN	QV9-NN1023-010600-189-h01 NN1023 Homo sapiens cDNA
10534	23569	37176	0.64	1.0E-36	AW85588.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.84	1.0E-36	AW856888.1	EST_HUMAN	RC3-CT0279-040600-017-e10 CT0279 Homo sapiens cDNA
11160	24259	37895	2.55	1.0E-36	AW897638.1	EST_HUMAN	CM3-NN0061-140400-147-r12 NN0061 Homo sapiens cDNA
11682	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	UHF-BN0-ale-o-03-o-01-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25029		10.8	1.0E-36	11646901	NT	Homo sapiens PPS227 protein (PPS227), mRNA
12340	26245		2.83	1.0E-36	11416177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12836	26556		6.76	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	29737		2.78	1.0E-36	AF202723.1	NT	Homo sapiens Sac1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80607.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7639	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80607.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12619	25417		3.57	9.0E-37	W22618.1	EST_HUMAN	7304 Human retina cDNA Tap509-cleaved subunitary Homo sapiens cDNA, not directional
3436	16604	28624	1.4	8.0E-37	4757979	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
6363	18566		1.7	8.0E-37	BE989077.1	EST_HUMAN	CM0-UT0003-050800-563-d39 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K0d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	MER28 repetitive element;
5968	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K0d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
8068	21160	34670	6.2	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1313	14469		4.82	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434E0422 5'
5228	18350	31320	3.04	7.0E-37	AW868823.1	EST_HUMAN	EST1780800 MAGC sequences, MAGJ Homo sapiens cDNA
10994	24073	37706	8.68	7.0E-37	AJ817700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
11134	24208	37831	1.80	7.0E-37	AJ536702.1	EST_HUMAN	PTR5 repetitive element;
8634	21714	35251	0.59	6.0E-37	AF168689.1	NT	h087g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
12884	25575		2.3	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternative isoform (PCDH-alpha10) mRNA, complete cds
12884	25641		4.5	6.0E-37	AF202723.1	NT	Human olfactory receptor cDNA17-201-1 (OR17-201-1) gene, olfactory receptor cDNA17-32 (OR17-32) gene and olfactory receptor pseudo cDNA17-01 (OR17-01) pseudogene, complete cds
6218	18393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sac1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6218	18393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
11160	24231		4.02	5.0E-37	7657117	NT	AV750211 NPC Homo sapiens cDNA clone NPC8GH09 5'
12335	25242		3.63	5.0E-37	AF149773.1	NT	Homo sapiens glycine C-acyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2495	19322	28741	2.97	4.0E-37	AA702794.1	EST_HUMAN	280b04.s1 Soares fetal_liver_spleen_1NRLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	19885	32947	0.68	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9558	22821	36192	0.66	4.0E-37	AA843806.1	EST_HUMAN	ak09ac02.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	18214	28332	3.42	3.0E-37	AL048856.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2074	18214	28333	3.42	3.0E-37	AL048856.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2581	17708		1.64	3.0E-37	AW981150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
3030	18208		4.02	3.0E-37	AW981150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
5885	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547G067 5'
7728	20780	34279	0.72	3.0E-37	A1749562.1	EST_HUMAN	ak34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TRCQ13637
302	19829	26666	0.89	2.0E-37	D89790.1	NT	Q13637 SIMILAR TO POGO ELEMENT ; Homo sapiens mRNA for AML1, complete cds
302	19829	26667	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AL131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1105	14270	27329	2.53	2.0E-37	AL131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28267	1.32	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3999	17159	30162	6.71	2.0E-37	4803210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebroside
4380	17503	30485	0.6	2.0E-37	4826685	NT	panthomatois), polypeptide 1 (GYP27A1b) mRNA
5504	18703		0.9	2.0E-37	BF035327.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DIDX1) mRNA
6076	19635	33224	0.6	2.0E-37	11690817	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:39862088 5'
6788	19553	33353	3.72	2.0E-37	AA349720.1	EST_HUMAN	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
8185	21267	34790	0.47	2.0E-37	BE537764.1	EST_HUMAN	EST62831 Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34791	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453957 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453957 5'
11856	24844	38541	10.07	2.0E-37	AF170013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
12797	25770		1.44	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
13184	25770		4.19	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2154	15280	28417	6.96	1.0E-37	AL165281.2	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
3267	16441		1.03	1.0E-37	AW862082.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
5065	18163	31159	2.34	1.0E-37	BF371719.1	EST_HUMAN	RC3-CT0347-210400-016-H03 CT0347 Homo sapiens cDNA
6127	19308		0.89	1.0E-37	7306360	NT	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
8408	21480	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	Mus musculus obogelin (Obog), mRNA
8933	22012	35551	3.59	1.0E-37	AA171406.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
							zpx21b02.r1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.12 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10937	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12871	25447		1.94	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0086-140700-243-d07 FT0086 Homo sapiens cDNA
5838	19086	32388	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain premyosin cytochrome protein Plocdo (LOC56768), mRNA
1249	14408	27470	1.96	8.0E-38	11436855	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
2587	15692	28817	1.21	8.0E-38	BF346221.1	EST_HUMAN	802018401F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4183982 5'
12735	14408	27470	1.37	8.0E-38	11436855	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
13210	26049		1.44	8.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2264	15387	28515	1.7	7.0E-38	AW972825.1	EST_HUMAN	EST384820 IMAGE resequences, MAGL Homo sapiens cDNA
3107	16283	29239	1.98	6.0E-38	BF030333.1	EST_HUMAN	601485722F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858348 5'
5706	18899	32192	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5706	18899	32193	0.88	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20557	34029	0.59	6.0E-38	8923130	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
12189	26147		4.27	8.0E-38	11436847	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
12704	25483	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
13160	25913	31861	1.79	6.0E-38	AW971819.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
745	13826	29867	0.9	5.0E-38	11418164	NT	Homo sapiens DNA for Human P2XM, complete cds
2625	16650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
3796	16957	29861	0.94	5.0E-38	7549804	NT	EST383908 IMAGE resequences, MAGL Homo sapiens cDNA
3971	16957	29861	0.77	5.0E-38	7549804	NT	Homo sapiens RUBIR gene (partial), exon 8
5288	15650	28774	0.98	5.0E-38	AJ237740.1	NT	Homo sapiens RUBIR gene (partial), exon 8
7172	20303	33748	1.93	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
121	13351	26380	4.28	4.0E-38	Z25486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z25486.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14346	27403	1.15	3.0E-38	11436847	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2187	15302		4.42	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-llc) (HIRIP4), mRNA
3958	17116	30119	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6863	26638	32453	6.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7393	20471	33937	0.58	3.0E-38	AW302461.1	EST_HUMAN	xw04d01 x1 NCI CGAP_Bim53 Homo sapiens cDNA clone IMAGE:2827009 3'
7763	20822	34313	6.53	3.0E-38	BF373964.1	EST_HUMAN	CM3-FT0181-140700-241-d07 FT0181 Homo sapiens cDNA
8851	21930	35499	2.11	3.0E-38	H85494.1	EST_HUMAN	yw68b04.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:249775 5'
8851	21930	35470	2.11	3.0E-38	H85494.1	EST_HUMAN	yw68b04.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:249775 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11588	24651		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11433947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
61	13290	26303	1.06	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14565	27639	3.66	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27814	13.95	2.0E-38	AA437353.1	EST_HUMAN	z3630401.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:70785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27815	13.95	2.0E-38	AA437353.1	EST_HUMAN	z3630401.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:70785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3622	16786		0.92	2.0E-38	AF070670.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17839	30824	18.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5282	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	z361400.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:788129 5' similar to TR:G817957
5838	19026	32331	0.75	2.0E-38	Z26634.2	NT	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5838	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20949	34467	1.47	2.0E-38	AV721103.1	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
8680	21760		4.47	2.0E-38	BE166890.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
9096	22176	35719	0.49	2.0E-38	F08450.1	EST_HUMAN	NR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9165	22243	35786	1.28	2.0E-38	AF069755.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
							Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22498		1.36	2.0E-38	BE222256.1	EST_HUMAN	h008902.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3160180 3' similar to TR:O02710 O02710
10665	23689	37309	1.67	2.0E-38	D63479.2	NT	GAG POLYPROTEIN ;
11781	24771	38467	4.86	2.0E-38	BE12780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0745 protein, partial cds
11939	24925	38626	2.88	2.0E-38	AF190501.1	NT	QV2-HT06898-080600-293-a05 HT06898 Homo sapiens cDNA
11939	24926	38627	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25188		6.21	2.0E-38	AV726988.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12246	25187		1.28	2.0E-38	AB012723.1	NT	AV726988 HTC Homo sapiens cDNA clone HTCAH-07 5'
12546	25370		3.36	2.0E-38	M55630.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12569	25381	32073	4.81	2.0E-38	HE5641.1	EST_HUMAN	Homo sapiens gene for kinesin-like protein, complete cds
12632	25426		2.87	2.0E-38	S74906.1	NT	Human topoisomerase I pseudogene 2
13174	25762		1.35	2.0E-38	11418248	NT	CHIR220390 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
							E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
							Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.96	1.0E-38	AA401570.1	EST_HUMAN	zu62802.r1 Sources_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
2055	15196	28310	2.82	1.0E-38	4885288	NT	MER19 repetitive element ;
2077	15217	28338	1.33	1.0E-38	7661689	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2564	15688	28815	1.89	1.0E-38	AF270631.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4271	17416	30405	0.93	1.0E-38	AB037863.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4439	17579	30558	0.6	1.0E-38	4505018	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30837	1.08	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
5268	18387	31355	1.89	1.0E-38	AL163280.2	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
6161	19327	32872	4.59	1.0E-38	7305360	NT	Homo sapiens chromosome 21 segment HS21C080
6151	19327	32873	4.59	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
7563	20635	34110	2.55	1.0E-38	AB014512.1	NT	Mus musculus obogelin (Obog), mRNA
8354	22429	35987	0.58	1.0E-38	11422250	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9810	22685	38236	6.31	1.0E-38	BES50127.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
12403	25877		4.79	1.0E-38	AL163284.2	NT	h09g01.x1 NCL CGAP_Kid19 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.t3
12116	25096	38801	1.84	9.0E-39	AA112438.1	EST_HUMAN	MER29 repetitive element ;
65	13284	28308	4.93	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1425	14579	27652	1.3	8.0E-39	4758228	NT	znt2707.r1 Stratiotes parviflorus (8337208) Homo sapiens cDNA clone IMAGE:526895 5'
1876	16020		1.8	8.0E-39	A1823404.1	EST_HUMAN	Homo sapiens ATRPase, H+ transporting, lysosomal (vacuolar proton pump) 16K0 (ATP6C) mRNA
2160	15296	28421	7.08	7.0E-39	AL163227.2	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
11047	24124	31768	2.4	6.0E-39	BF331829.1	EST_HUMAN	wh33110.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
13064	25697		2.24	6.0E-39	BE670394.1	EST_HUMAN	POL PROTEIN ;
1032	14201	27269	1.84	5.0E-39	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C027
3050	16228	28247	9.33	5.0E-39	A1750154.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
12720	25479		1.53	6.0E-39	11420289	NT	QY1-BT0631-040800-357-02 BT0631 Homo sapiens cDNA
							7e94cd3.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP.R151.6
							CE00828 ;
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							et38b04.x1 Barcode colon HFLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
							Q16408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.t1 LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
564	13755	26762	4.39	4.0E-39	AB015610.1	NT	Chlorobacter ethiops mRNA for ribosomal protein S4X, complete cds
3663	18626	20835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	16138	32460	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5950	16138	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA682948.1	EST_HUMAN	ac22g04.s1 Striatogene echizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9530	22595	36165	0.46	4.0E-39	DB4116.1	NT	OPRL1 ORF repetitive element;
9530	22595	36166	0.46	4.0E-39	DB4116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25404		6.36	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12884	25666		2.58	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
48	13287	26297	11.98	3.0E-39	AA631849.1	EST_HUMAN	QV6-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
48	13287	26298	11.96	3.0E-39	AA631849.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26299	11.96	3.0E-39	AA631849.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38348	6.59	3.0E-39	A084657.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38349	6.59	3.0E-39	A084657.1	EST_HUMAN	alpha3a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1600988 3' similar to SW:GTR5_RAT
12284	25212		5.72	3.0E-39	H37803.1	EST_HUMAN	alpha3a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1600988 3' similar to SW:GTR5_RAT
920	14095		7.78	2.0E-39	BE408203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
935	14110		11.65	2.0E-39	A1525119.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
1057	14223		3.9	2.0E-39	AF000573.1	NT	9p51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
1560	14713		33.58	2.0E-39	AW372318.1	EST_HUMAN	601801607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638289 5'
2030	15171	26279	4.48	2.0E-39	AA720574.1	EST_HUMAN	promme-7 D01.1 brain tumor Homo sapiens cDNA 5'
2682	15812	26828	1.88	2.0E-39	AL163248.2	NT	Homo sapiens homogenisate 1 2-dioxygenase gene, complete cds
4523	17662	30649	1.74	2.0E-39	BF370207.1	EST_HUMAN	PM0-BT0340-211290-003-462 BT0340 Homo sapiens cDNA
5608	18603	31868	4.45	2.0E-39	AA608880.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
7528	20569	34073	2.06	2.0E-39	AA608880.1	EST_HUMAN	THR repetitive element;
7702	20767	34251	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C0048
7702	20767	34252	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C0048
8505	21568	36120	0.63	2.0E-39	AF078770.1	NT	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
9826	22666		0.79	2.0E-39	AF068660.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
11716	24756	38452	2.13	2.0E-39	DB6984.1	NT	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
1543	14695	27774	2.83	1.0E-39	AJ006345.1	NT	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1643	14695	27775	2.63	1.0E-39	AJ00345.1	NT	Homo sapiens KVLQ11 gene
1651	14714	27781	5.98	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1763	14812	28007	1.14	1.0E-39	H65224.1	EST_HUMAN	Chr220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17817	30903	9.32	1.0E-39	AW851895.1	EST_HUMAN	EST384065 MAGC resequences, MAG8 Homo sapiens cDNA
4782	17817	30904	9.32	1.0E-39	AW851895.1	EST_HUMAN	EST384066 MAGC resequences, MAG8 Homo sapiens cDNA
4824	17857	30943	9.13	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5474	18673	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18673	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	y428g08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains
5781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Alu repetitive element contains LTR1 repetitive element
5781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6985	20193	37867	1.95	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7621	20694	34069	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8782	21841	35382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11165	24236	37867	1.4	1.0E-39	4758051	NT	Homo sapiens ribosomal protein S6 kinase, 80kD, polypeptide 5 (RPS8KA5) mRNA
668	13781	28785	2	8.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4756145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27485	16.02	9.0E-40	4756145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
3885	17044	30043	1.18	9.0E-40	4503764	NT	mRNA
4081	18487	30242	3.89	9.0E-40	AB033070.1	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4466	17806	30884	5.63	9.0E-40	4507848	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3106	16282	28288	1.04	8.0E-40	AA078165.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
4033	17189		3.43	8.0E-40	BE36541.1	EST_HUMAN	7H15A04 Chromosome 7 HcLa cDNA Library Homo sapiens cDNA clone 7H15A04
							601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618168 5'
7894	20846	34452	2.21	7.0E-40	U80325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20846	34453	2.21	7.0E-40	U80325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2789	19004	28011	9.91	8.0E-40	AA361275.1	EST_HUMAN	EST70627 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
2788	19004	28012	9.91	8.0E-40	AA361276.1	EST_HUMAN	EST70627 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
6060	16242		1.85	6.0E-40	BE504786.1	EST_HUMAN	h240g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6276	19449		1.38	8.0E-40	7681988	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7076	20128	33544	3.04	6.0E-40	11438783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33546	3.04	6.0E-40	11438783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	8.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDDGF04 3'
10182	23219	36812	6.09	8.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDDGF04 3'
2670	15791	28907	2.75	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1925	16068	28173	3.91	4.0E-40	AI686005.1	EST_HUMAN	h91101.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL_PROTEIN.1
2175	15310		6.91	4.0E-40	AF009628.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17647	30635	7.2	4.0E-40	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.84	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	m34e10.1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10555	24038	37671	1.96	4.0E-40	AW841595.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17388	30385	0.9	3.0E-40	AB228949.1	EST_HUMAN	vt1287.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2380549 3'
4993	18122	37615	0.83	3.0E-40	AA055118.1	EST_HUMAN	z16f09.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377163 3'
6592	18752	33137	0.86	3.0E-40	4508738	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RP-S6K81) mRNA
6777	19332	33328	7.08	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.86	3.0E-40	6464167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	22247	35780	1.27	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22488	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D86064.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24000	38278	9.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI223036.1	EST_HUMAN	q952408.x1 Soares_lesfs_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13996		5.58	2.0E-40	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW-RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S6.1

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1888	15130	28233	2.6	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1988	16130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15258	28389	1.39	2.0E-40	A1968562.1	EST_HUMAN	W80a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q81829 Q81829
2238	15371	28500	2.21	2.0E-40	5453592	NT	ZINC FINGER PROTEIN.
2754	15871		1.66	2.0E-40	BE276932.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
3196	16371	28378	5.27	2.0E-40	5453592	NT	801121587F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3945784 5'
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
806	14061		1.2	1.0E-40	AA225689.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2886	15806	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	nc039a09.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007608
2760	15867		3.88	1.0E-40	BE018348.1	EST_HUMAN	601460375F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3963803 5'
3370	16542		2.14	1.0E-40	4507142	NT	b67a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048670 5' similar to TR:Q82168 Q82168
4733	17868	30851	3.69	1.0E-40	4508012	NT	SYNTAXIN 17.
6385	19554	32912	0.68	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens sorting nexin 3 (SNX3) mRNA
6385	19554	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7381	20458	33922	0.82	1.0E-40	P28808	SWISSPROT	tt42604.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'
11157	24228	37858	8.41	1.0E-40	AU149345.1	EST_HUMAN	tt42604.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'
11993	24978	38683	1.49	1.0E-40	AA614255.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
11993	24978	38684	1.49	1.0E-40	AA614255.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
12079	25059		1.88	1.0E-40	AL163246.2	NT	np08h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136408
1287	29032		6.94	1.0E-40	BF334112.1	EST_HUMAN	G1136408 KIAA0173 PROTEIN.
3808	17065	30064	0.58	9.0E-41	W01698.1	EST_HUMAN	np08h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136408
8106	21188	34708	1.6	8.0E-41	AL163203.2	NT	G1136408 KIAA0173 PROTEIN.
851	18024	27089	2.62	7.0E-41	AL834364.1	EST_HUMAN	np08h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136408
851	16024	27090	2.52	7.0E-41	AL834364.1	EST_HUMAN	G1136408 KIAA0173 PROTEIN.

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6379	18681	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6132	16311	32651	2.71	7.0E-41	11418208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6483	18650	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	UT2335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11718	24758	38453	2.06	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11831	24917	38620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028		8.58	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	8.0E-41	AB037183.1	NT	Homo sapiens DSCR5b, mRNA, complete cds
2179	15314	28443	3.09	8.0E-41	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8158	21240	34760	1.31	8.0E-41	BF513783.1	EST_HUMAN	UIH-BW1-amp-b-03-0-JLs1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13158	25952		1.25	8.0E-41	AW873637.1	EST_HUMAN	trc4498.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.B3 MER32 repetitive element;
1845	14991	28082	1.37	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:78626 3'
4223	17371		1.17	5.0E-41	4885686	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6878	18937		2.34	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251189-002-F11 BT0341 Homo sapiens cDNA
402	13699		1.69	4.0E-41	BE158318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU118344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
1442	14595	27870	14.6	4.0E-41	A027117.1	EST_HUMAN	ow45e08.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1442	14595	27671	14.6	4.0E-41	A027117.1	EST_HUMAN	ow45e08.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1454	14607	27887	3.34	4.0E-41	AB009881.1	NT	Homo sapiens gene for actin receptor type IIB, complete cds
1685	14817	27900	7.72	4.0E-41	A1500408.1	EST_HUMAN	trc6604.x1 NCL CGAP_Birt25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2953	16130	29144	5.02	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
2953	16130	29146	5.02	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4262	17407	30393	2.13	4.0E-41	X92885.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
6838	19797		1.8	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
8895	22935	36519	5.06	4.0E-41	BF304883.1	EST_HUMAN	60188808F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11969	24954		7.38	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
13110	25725	31942	1.61	4.0E-41	BE88718.1	EST_HUMAN	G01508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
970	14143	27203	1.3	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4456	17593	30575	4.03	3.0E-41	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6609	18804	31869	11.78	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6511	19676	33048	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7987	21017	34329	0.71	3.0E-41	R54765.1	EST_HUMAN	Y75508.r1 Soares breast 2NtHBst Homo sapiens cDNA clone IMAGE:154575 5'
12118	26099	38804	1.38	3.0E-41	AW694941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12119	26099	38805	1.38	3.0E-41	AW694941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12106	25163		1.98	3.0E-41	AA609768.1	EST_HUMAN	af17710.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	G01762840F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15163	28258	2.17	2.0E-41	AA931940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2293	15425	28359	1.26	2.0E-41	D86882.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	16472	28606	5.52	2.0E-41	X89631.1	NT	G. gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	29501	0.69	2.0E-41	AA448549.1	EST_HUMAN	z08604.r1 Soares fetal N22HF8_9w Homo sapiens cDNA clone IMAGE:788839 5'
3941	17100	30097	0.69	2.0E-41	5032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17879	30862	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17878	30863	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5856	18850	32132	0.6	2.0E-41	AA594575.1	EST_HUMAN	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6763	19919	33314	0.98	2.0E-41	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
7850	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (Nedd5) mRNA, complete cds
8269	21341	34858	1.38	2.0E-41	M66944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8269	21341	34859	1.38	2.0E-41	M66944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8268	21370	34891	1.42	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9176	22263	35798	1.65	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 136
9617	22672	36241	0.68	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11776	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13148	25747		1.2	2.0E-41	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
3278	18460	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	G01445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	16450	29471	1.05	1.0E-41	BE868735.1	EST_HUMAN	501445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17624	30811	9.46	1.0E-41	6878468	NT	Mus musculus tubulin alpha 6 (Tub6), mRNA
9618	22673	36243	1.57	1.0E-41	AI217668.1	EST_HUMAN	qf75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1756858 3'
12334	25241		1.67	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21787		1.19	9.0E-42	BE179191.1	EST_HUMAN	RC0-H10613-210300-032-g01 HT0613 Homo sapiens cDNA
9375	22450	36011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9375	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
475	13670	28702	5.34	8.0E-42	AF003630.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2178	16311	28439	8.63	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12375	28035		30.09	8.0E-42	AA469896.1	EST_HUMAN	h07c02.61 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943588 similar to TR:G434304 G434304 3'UTR EXPRESSED SEQUENCE TAG MRNA:
12396	25904		2.91	8.0E-42	AW088062.1	EST_HUMAN	3c97a04.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2692174 3' similar to contains ORF.L2
855	14128		2.23	7.0E-42	AL163285.2	NT	ORF repetitive element:
8688	21746		0.5	7.0E-42	R10963.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9445	22561	36124	1.32	7.0E-42	AI204568.1	EST_HUMAN	Y08904.J1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129174 5'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	qf58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2383	15494		3.6	6.0E-42	AW288658.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
5584	18779	31824	1.55	6.0E-42	AB026890.1	NT	3c20f08.x1 NCI_CGAP_HIN10 Homo sapiens cDNA clone IMAGE:2741788 3' similar to contains L1.L1
5834	18779	31824	1.5	6.0E-42	AB026890.1	NT	repetitive element:
138	13364		6.34	6.0E-42	AJ271735.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
451	13847	26883	1.56	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
499	13694		3.05	6.0E-42	5730038	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
500	13695		1.14	5.0E-42	5730038	NT	h031e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
6825	18978	33385	0.94	5.0E-42	11433063	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6825	18978	33389	0.94	5.0E-42	11433063	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6941	20254	33691	2.57	5.0E-42	11417857	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBES3A), mRNA
7351	20430	33882	1.55	5.0E-42	AF071589.1	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBES3A), mRNA
							Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
							Homo sapiens multifunctional catenulin/modulin-dependent protein kinase II delta2 isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8878	22057	35589	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24316	37855	1.77	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF055088.1	NT	Homo sapiens MHC class I region
772	13953	27003	5.6	4.0E-42	AF055088.1	NT	Homo sapiens MHC class I region
1091	14256	27312	1.82	4.0E-42	AF188011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4343	17486	30469	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAC mRNA, complete cds
4344	17507	30488	4.67	4.0E-42	4506498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RF4) mRNA
4706	17941	30825	17.04	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5285	18404	31372	0.93	4.0E-42	7061635	NT	Homo sapiens DKFZP684O2082 protein (DKFZP684O2082), mRNA
10701	23734	37336	0.57	4.0E-42	AW371201.1	EST_HUMAN	CNO-BT0282-171289-127-403 BT0282 Homo sapiens cDNA
10884	23868	37697	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-040400-018-111 ST0278 Homo sapiens cDNA
10884	23868	37698	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-040400-018-111 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AK45225.1	EST_HUMAN	h11402.x1 NCL_OGAP_Par1 Homo sapiens cDNA clone IMAGE:2130147 3'
11688	24885	38387	1.69	4.0E-42	BF035327.1	EST_HUMAN	601468631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1512	14885	27750	3.78	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2466	16593	28718	1.6	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKG Homo sapiens cDNA clone CKGC8308 5'
2483	15910		4.24	2.0E-42	AW693344.1	EST_HUMAN	RC3-NN0070-270400-011-110 NN0070 Homo sapiens cDNA
2496	15923	28742	3.6	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5876	19065	32372	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST387488 MAGE resequencing, MAGEC Homo sapiens cDNA
5876	19065	32373	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST387488 MAGE resequencing, MAGEC Homo sapiens cDNA
6892	20044	33452	0.9	2.0E-42	AK052586.1	EST_HUMAN	ow63005.x1 Soares_fetal_liver_epilepsy_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1663417 3'
10048	23084	36685	1.28	2.0E-42	BE538918.1	EST_HUMAN	801061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23295	36892	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
10260	23295	36893	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
12037	25019	38723	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
762	13632	26977	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pTIE-1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW295809.1	EST_HUMAN	U1H-B1-aff-e-04-0-J1.st NCL_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14290	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14290	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	18033	27498	11.98	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homodog mRNA, nuclear gene encoding mitochondrial protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1271	18033	27499	11.99	1.0E-42	AF067188.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1735	14884	27977	1.15	1.0E-42	11423219	NT	Homo sapiens nec (LOC51201), mRNA
2087	15227	28349	1.18	1.0E-42	AF110298.1	NT	Homo sapiens PDNP1 gene, exon 17
2809	15733	28849	1.42	1.0E-42	5174468	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3029	16205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCL5) mRNA, and translated products
3789	16960	29964	3.31	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3895	17054	30064	1.11	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
4038	17162	30202	0.99	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4716	17651	30834	0.91	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-003 ST0197 Homo sapiens cDNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4801	18031	31020	6.13	1.0E-42	4806768	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
11440	24501	38189	1.39	1.0E-42	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:368310 5'
10291	23326	36929	8.16	9.0E-43	4757689	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
689	13855	26883	20.77	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
689	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
718	13900	26938	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5816	19008	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	y09e11.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:148172 5'
3731	16892	29898	7.48	7.0E-43	AW246442.1	EST_HUMAN	2822251 Spriime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8988	22047		3.98	7.0E-43	A1936748.1	EST_HUMAN	w098d01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468865 3' similar to TRO15475
1374	14529		11.82	6.0E-43	AA491890.1	EST_HUMAN	O16475 UNNAMED HERV-H PROTEIN contains LTR7.b1 LTR7 repetitive element;
2657	15780		4.03	9.0E-43	AV708201.1	EST_HUMAN	me72d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:308803 similar to gb-L05085 80S
4983	18092	31068	252.27	6.0E-43	A1421540.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6441	18608	32971	2.63	6.0E-43	9955973	NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
							tt28d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2097318 3' similar to SW-BRR2_YEAST
							P32639 PRE-MRNA SPLICING HELICASE BRR2;
							Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP-3B, mRNA

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7048	20101	39518	1.8	6.0E-43	AW488897.1	EST_HUMAN	h488894.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810881 3' similar to contains MER1.13 MER1 MER1 repetitive element;
10056	23094	36038	1.77	6.0E-43	AA195164.1	EST_HUMAN	z35a06.r1 Soares_NHL-MPU_S1 Homo sapiens cDNA clone IMAGE:065410 5' similar to TR:G528641
11383	24624		2.45	6.0E-43	AL119153.1	EST_HUMAN	G528641 DB1, COMPLETE CDS, contains element PTR7 repetitive element;
145	13370		1.82	5.0E-43	AL163213.2	NT	DKFZp781L1712_1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L1712 5'
515	13709	28738	3.4	5.0E-43	AA382780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2808	16086	28100	1.99	5.0E-43	AV732578.1	EST_HUMAN	EST186033 Testis 1 Homo sapiens cDNA 5' and
6435	20098	33512	0.9	5.0E-43	AI613508.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
7043	20096	33512	0.89	5.0E-43	AI613509.1	EST_HUMAN	hw22a07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280452 3'
8381	21482	34985	0.84	5.0E-43	AA442271.1	EST_HUMAN	hw22a07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280452 3'
8381	21482	34986	0.84	5.0E-43	AA442271.1	EST_HUMAN	z35a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22169		0.73	5.0E-43	H74277.1	EST_HUMAN	z35a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9594	22708	36272	4.09	5.0E-43	AA465288.1	EST_HUMAN	y449g12.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:228610 5'
10608	23643	37251	2.6	5.0E-43	AI733244.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10651	23685	37285	1.02	5.0E-43	AL049110.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
11213	24282	37621	2.24	5.0E-43	W29011.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
886	15987	27227	4.4	4.0E-43	AF003528.1	NT	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
5373	18576	31444	1.09	4.0E-43	AI050338.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
6489	18665	33028	0.68	4.0E-43	6998009	NT	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
7280	20363		1.8	4.0E-43	11418783	NT	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
8371	21482	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
8371	21452	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10521	23556	37184	1.02	4.0E-43	6005967	NT	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
12311	25227		2.7	4.0E-43	R20650.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
13030	25898		1.33	4.0E-43	AI436093.1	EST_HUMAN	ss33403.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14880	27971	2.52	3.0E-43	X07869.1	NT	H. sapiens gene encoding La autoantigen
2120	18065	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp82f01.1 Scores fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:183948 5' similar to contains MSR1 repetitive element;
3682	18825	28834	1.22	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein [rearranged translocation] (human, leukemic cell line SKHL, mRNA Mutant, 5838 nt)
4405	17548	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	h155d06.s1 NCI_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017419
6014	19198	32515	0.94	3.0E-43	D34813.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	19654	33016	1.56	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
6487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
6867	20019	33428	5.09	3.0E-43	U85487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa38f11.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
9020	22089	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10088	23106	36709	0.88	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbonyltransferase (H. sapiens) (LOC83848), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETIMAR) mRNA
188	13410		7.24	2.0E-43	A180764.1	EST_HUMAN	q61c09.x1 Scores testis, NIH Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
6804	19764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	h153a08.x1 NCI_CGAP_Bim41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
6804	19764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	h153a08.x1 NCI_CGAP_Bim41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7426	20503	33973	1.29	2.0E-43	AW207390.1	EST_HUMAN	U1H-B11-af-a-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8503	21584		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11476	24835		4.75	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1681	14833	27917	2.96	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3' and similar to LINE-1
1681	14833	27918	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27985	4.12	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2768	15902	28009	4.73	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5526	18173	31740	0.89	1.0E-43	4885544	NT	602022313F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157888 6'
6744	19900	33291	6.84	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19900	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7109	18533	31488	1.19	1.0E-43	R19751.1	EST_HUMAN	y940c01.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
8117	21189	34720	0.6	1.0E-43	AF176285.1	NT	SP-BD38_MOUSE P28658 BRAIN PROTEIN DN38 ;
8266	21338		2.17	1.0E-43	AF188490.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
9037	22116	35659	28.54	1.0E-43	AW863676.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTG8 (CBFAZT1) gene, partial cds
10498	23633	37143	0.66	1.0E-43	AW853229.1	EST_HUMAN	EST1375749 IMAGE: ressequences, MAGH Homo sapiens cDNA
11206	24275	37812	6.81	1.0E-43	AI884961.1	EST_HUMAN	EST1365289 IMAGE: ressequences, MAGH Homo sapiens cDNA
11847	24728	38418	3.05	1.0E-43	11424978	NT	w87h01.x1 NCL CGAP_KU111 Homo sapiens cDNA clone IMAGE:2494705 3'
12248	25189		2.29	1.0E-43	AL137984.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CAGNA1E), mRNA
12550	25373	32071	3.16	1.0E-43	AI675416.1	EST_HUMAN	DKFZp781D1015.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp781D1015 5'
12805	25538	32013	3.21	9.0E-44	11418322	NT	w66b04.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3'
913	14088	27163	5.32	8.0E-44	AI222385.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	14088	27154	6.32	8.0E-44	AI222385.1	EST_HUMAN	q123g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8736	21815	35350	2.86	8.0E-44	X94354.1	NT	q123g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
10546	23580	37189	0.5	8.0E-44	11423497	NT	H. sapiens DNA for Cone cGMP-PDE gene
10545	23580	37190	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38877	2.87	8.0E-44	Y10488.2	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11887	24972	38877	1.76	8.0E-44	L29139.1	NT	Homo sapiens mRNA for tyrosine kinase, partial cds
12601	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens myosin mRNA, partial cds
12544	25735	31946	2.17	8.0E-44	11418088	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12945	25938	31780	1.85	8.0E-44	11418039	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
13126	25735	31946	2.29	8.0E-44	11418088	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
676	13862		1.13	7.0E-44	R06035.1	EST_HUMAN	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
2307	15439	28573	1.19	7.0E-44	6031888	NT	y689e01.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124820 5'
3031	16207	28228	4.44	7.0E-44	AF048728.1	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	28230	4.44	7.0E-44	AF048728.1	NT	Homo sapiens minisatellite ms32 repeat region
3985	17123	30126	2.71	7.0E-44	AL163284.2	NT	Homo sapiens minisatellite ms32 repeat region
4366	17499	30479	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 segment HS21C084
4366	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21460	34963	2.39	7.0E-44	AF231919.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
6229	19404	32754	0.67	6.0E-44	AU169839.1	EST_HUMAN	AU169839 Y79AA1 Homo sapiens cDNA clone Y79AA1000493 3'
314	13530		4.25	5.0E-44	AL289380.1	NT	HSAADDEYUP, Human fetal Brain Whole tissue Homo sapiens cDNA
342	13553		2.42	5.0E-44	AJ289380.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34873	4.12	5.0E-44	AI598523.1	EST_HUMAN	tr40d02.x1 NC1_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11 OFR OFR repetitive element :
9584	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3501	16668	29678	4.27	4.0E-44	AL163033.2	NT	Homo sapiens chromosome 21 segment HS21C103
5126	18253		0.89	4.0E-44	AI432226.1	EST_HUMAN	311402.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
7639	20708	34187	0.67	4.0E-44	BE8683178.1	EST_HUMAN	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8468	21547	36077	0.88	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
8078	22158		0.71	4.0E-44	BE176818.1	EST_HUMAN	RC3-HT0585-010400-023-408 HT0585 Homo sapiens cDNA
11513	24570	38247	5.64	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (GLIM1) mRNA, complete cds
1827	14976		1.5	3.0E-44	6912477	NT	Homo sapiens karyophenin alpha 6 (impartin alpha 7) (KFNAB6). mRNA
3167	16342	29350	5.11	3.0E-44	AA169851.1	EST_HUMAN	2p18k05.11 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
7970	21020	34533	0.63	3.0E-44	BE584820.1	EST_HUMAN	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
9719	22784	36355	0.63	3.0E-44	AF003273.1	NT	Sus scrofa domestica submaxillary epimucins mRNA, complete cds
1074	14240	27286	1.43	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1074	14240	27297	1.43	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14393	27455	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21). mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21). mRNA
1340	14496	27588	6.92	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2219	15353	28494	9.07	2.0E-44	AF070651.1	NT	P220399 OXYSTEROL-BINDING PROTEIN. :
2605	15728		1.20	2.0E-44	4507582	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2642	15785	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2676	15796		2.3	2.0E-44	5901933	NT	Human mRNA for integrin alpha subunit, complete cds
3559	16724	28740	1.34	2.0E-44	D87875.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4). mRNA
4882	17827	30813	1.75	2.0E-44	AW884378.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6220	18396	32744	1.75	2.0E-44	11446801	NT	PM4-SN0016-120500-003-404 SN0016 Homo sapiens cDNA
6220	18396						Homo sapiens chemokine (C-C motif) receptor 8 (CCR8). mRNA
6220	18396						Homo sapiens general transcription factor 2-1 (GTF2) mRNA, alternatively spliced product, complete cds
7572	20844	34121	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3). mRNA
7572	20844	34122	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3). mRNA
8823	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817). mRNA
8823	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817). mRNA
8819	21898	35437	1.8	2.0E-44	BE388058.1	EST_HUMAN	80128974F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3913586 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12162	26122		4.59	2.0E-44	BE244602.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylce-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.56	2.0E-44	4826963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
63	13262	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
63	13262	26307	5.24	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
594	13784	26804	1.63	1.0E-44	AW853192.1	EST_HUMAN	RC1-CT0249-030300-028-112 CT0249 Homo sapiens cDNA
1224	14384		1.96	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1605	14758		8.06	1.0E-44	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2269	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53d02.1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.3 THR repetitive element;
2299	19431	28364	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53d02.1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.3 THR repetitive element;
2818	16932	28043	1.74	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, AA differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3819	16978		3	1.0E-44	AA455889.1	EST_HUMAN	es01c08.s1 Scores: NIHMPU_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5221	18343	31314	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequenced, MAGJ Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequenced, MAGJ Homo sapiens cDNA
8848	21927	35468	0.96	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.56	1.0E-44	AJ337183.1	EST_HUMAN	q888g07.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2008628 3'
11284	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCB8Y503 5'
11820	24809	38505	3.47	1.0E-44	10082684	NT	Homo sapiens Sush domain (SCR repeat) containing (BK65A8.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150889-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150889-011-C08 CT0198 Homo sapiens cDNA
4701	17839	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4701	17839	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
6787	18842	33340	1.41	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0905 protein, partial cds
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	18915	31263	0.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21980	34902	1.03	8.0E-46	AA377885.1	EST_HUMAN	EST80883 Synovial sarcoma Homo sapiens cDNA 5' end
1583	14735		2.36	6.0E-45	AN675425.1	EST_HUMAN	wh88c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element;

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83107.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12911	26164		1.89	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	14090		1.71	6.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058	15189	28313	4.42	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-615-F01 CN0044 Homo sapiens cDNA
3281	18455	28477	2.87	6.0E-45	AI523768.1	EST_HUMAN	ig94f07.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
5629	18823	31897	8.95	5.0E-45	AA397781.1	EST_HUMAN	P09084 PAIRED BOX PROTEIN PAX-1;
6143	19321	32684	1.09	5.0E-45	Y18933.1	NT	z172d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element
6143	19321	32685	1.09	5.0E-45	Y18933.1	NT	TAR1 repetitive element;
6190	19366	32714	0.92	5.0E-45	AB022318.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens MCP-1 gene and enhancer region
6318	19480	32847	0.87	5.0E-45	11496268	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19490	32848	0.87	5.0E-45	11496268	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8241	22318	35861	1.45	5.0E-45	4759223	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
11697	24082	36888	2.5	5.0E-45	8923688	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
1167	14330	27385	6.3	4.0E-45	X95828.1	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
2365	15496	28622	2.15	4.0E-45	BE266622.1	EST_HUMAN	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
9157	22235		0.81	4.0E-45	AA226220.1	EST_HUMAN	Homo sapiens programmed cell death 5 (PDCD5), mRNA
12166	23080	31650	1.36	4.0E-45	11435947	NT	Homo sapiens golgi-like protein (GLP), mRNA
3411	16590		0.93	3.0E-45	T71480.1	EST_HUMAN	H1.sapiens ART14 gene
4199	16590		1.03	3.0E-45	T71480.1	EST_HUMAN	601194440F-1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
6368	19538	32895	1.34	3.0E-45	6753651	NT	repetitive element;
6366	19536	32896	1.34	3.0E-45	6753651	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
8645	21725		1.76	3.0E-45	AV723976.1	EST_HUMAN	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
8991	22070	35810	4.31	3.0E-45	4738481	NT	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
10515	23650	37169	7.52	3.0E-45	AL163227.2	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
10515	23650	37160	7.52	3.0E-45	AL163227.2	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
13040	26078		3.45	3.0E-45	X89211.1	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
2572	16597		3.12	2.0E-45	AL163218.2	NT	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
3097	16273	28287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6651	16810	33198	5.45	2.0E-45	U01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7766	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8610	21690	35228	0.91	2.0E-45	AW634834.1	EST_HUMAN	RCOL T0001-150200-032-d11 LT0001 Homo sapiens cDNA
9784	22824	36402	0.51	2.0E-45	AW636786.1	EST_HUMAN	ts56a01.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2232552 3'
11042	25867	37764	12.66	2.0E-45	BE934350.1	EST_HUMAN	MF0-H70923-160800-201-a02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa87712.11 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144669 G1144568 R-SLY1.
11784	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
11784	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13087	25710		2.73	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
126	13617		1.22	1.0E-45	BE388855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
422	13617		1.99	1.0E-45	BE388855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
485	13678	26714	1.02	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1201	14363	27423	1.68	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3172	16347	29354	10.41	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3581	16746	29764	0.85	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3684	16927	29836	0.69	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4589	17736	30716	6.4	1.0E-45	BE396633.1	EST_HUMAN	601289110F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618603 5'
4948	17981		1.05	1.0E-45	H67443.1	EST_HUMAN	y05002.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
5081	18209	31181	1.56	1.0E-45	11545798	NT	Homo sapiens ribon protein (NIBAN), mRNA
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8806	21885	35426	0.9	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9321	22367	35850	3.92	1.0E-45	BE887843.1	EST_HUMAN	601511225F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9722	22767	36358	0.99	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12369	25263	32117	3.5	1.0E-45	11418068	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12668	26384		19.43	1.0E-45	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12668	26387		6.42	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
13047	25696	31663	4.02	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8423	21504	35037	2.71	9.0E-46	8910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8835	21914		6.52	9.0E-46	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
10687	23730	37335	6.89	9.0E-46	AW246884.1	EST_HUMAN	2822448.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	A1433261.1	EST_HUMAN	U32708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
							TUBULIN BETA-1 CHAIN (HUMAN);
2513	15639	28761	7.67	8.0E-46	A1433261.1	EST_HUMAN	U32708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
8244	21328		2.72	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4703	17838		4.79	7.0E-46	BE386165.1	EST_HUMAN	RCS-HT0508-280/200-012-C12 HT0506 Homo sapiens cDNA
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	601277292F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3818119 5'
6167	19343	32689	4	7.0E-46	8822708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6623	19783	33171	1.8	7.0E-46	BF105945.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
12708	25488		2.6	7.0E-46	AL163246.2	NT	601822835F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4042736 5'
							Homo sapiens chromosome 21 segment HS21C046
2812	15928	29037	6.87	6.0E-46	A1884381.1	EST_HUMAN	Wnt31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2812	15928	29038	6.87	6.0E-46	A1884381.1	EST_HUMAN	Wnt31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437576 3' similar to contains MER19.12
							MER19 repetitive element;
							MER19 repetitive element;
6257	19431	32778	11.57	6.0E-46	A1636448.1	EST_HUMAN	Wnt31f08.x1 NCI_CGAP_Kd8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
							SA GENE.;
7386	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	Xp42a04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2706664 3' similar to gb:L08069 DNAJ
7541	20514	34091	0.87	6.0E-46	BF509740.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	U1H-B14-epg-b-08-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
209	13432		6.31	6.0E-46	AL163210.2	NT	601479409F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3880985 5'
3617	16781	29798	1.17	5.0E-46	BE677194.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3617	16781	29797	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6874	20028	33436	1.52	5.0E-46	BF590442.1	EST_HUMAN	nas38807.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
7080	20174	33598	3.89	5.0E-46	BF347228.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7244	20327	33772	0.75	6.0E-46	AW582253.1	EST_HUMAN	602021184F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4156670 5'
7544	20516	34093	0.59	6.0E-46	BE549744.1	EST_HUMAN	QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA
							7b38b05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
							no54e08.s1 NCI_CGAP_S31 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1740	14889	27981	2.99	4.0E-46	AW770544.1	EST_HUMAN	H186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14880	27982	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:U14008_ma1
2788	15913	29021	7.4	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
5553	18750	31786	2.1	4.0E-46	M36852.1	NT	Human endogenous retrovirus RTVL-H2
5553	18750	31787	2.1	4.0E-46	M36852.1	NT	Human Ig gamma chain gene V region, partial cds
12851	25565	31980	1.38	4.0E-46	M36852.1	NT	Human Ig gamma chain gene V region, partial cds
2359	15490	28920	0.94	3.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4513	17652	30840	1.21	3.0E-46	7857203	NT	Homo sapiens acidic 82 kDa protein mRNA (HISU16552), mRNA
4898	18028	31015	1.11	3.0E-46	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP4K3), mRNA
4898	18028	31016	1.11	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line, Ig-Light-Lambda; VLambda
8949	22028	35569	12.45	3.0E-46	A1831462.1	EST_HUMAN	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line, Ig-Light-Lambda; VLambda
9206	22284	35824	0.61	3.0E-46	L08850.1	NT	wf9c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contig THRLb2
9206	22284	35825	0.61	3.0E-46	L08850.1	NT	THR repetitive element;
11873	24861	38556	1.78	3.0E-46	D31785.1	NT	Human AD amyloid mRNA, complete cds
860	14037	27099	12.65	2.0E-46	AA468846.1	EST_HUMAN	Human AD amyloid mRNA, complete cds
1593	14746		3.78	2.0E-46	AA678246.1	EST_HUMAN	Human AD amyloid mRNA, complete cds
1671	14823	27906	5.63	2.0E-46	U78027.1	NT	Human mRNA for KIAA0081 gene, partial cds
6089	18217	31188	1.26	2.0E-46	AA389286.1	EST_HUMAN	ne08a09.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:380408 3' similar to contains THR.b2 THR
7653	20721	34197	7.1	2.0E-46	9810569	NT	repetitive element;
8260	21342		1.29	2.0E-46	BE869161.1	EST_HUMAN	z27a1.1.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431868 3'
11524	24990		1.82	2.0E-46	7857233	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
12294	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
12555	25031		1.57	2.0E-46	H468391.1	EST_HUMAN	z59a02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-RSP1_MOUSE
12596	25401		3.31	2.0E-46	AA001786.1	EST_HUMAN	Q01730 RSP-1 PROTEIN.;
12834	25923	31864	4.28	2.0E-46	AW27214.1	EST_HUMAN	Mus musculus sperm tail associated protein (Stap), mRNA
1281	14418	27483	4.31	1.0E-46	4502894	NT	801445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
2356	15487	28619	4.88	1.0E-46	AW978516.1	EST_HUMAN	Homo sapiens small acidic protein (IMAGE145052), mRNA
							601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997328 5'
							y32b01.r1 Scores_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:206977 5'
							zh84f12.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428016 5'
							xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
							Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
							EST350625 IMAGE:resequences, MAGP Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST485085 WATM1 Homo sapiens cDNA clone 485085
3321	16494	29511	2.12	1.0E-46	AA631012.1	EST_HUMAN	np78502.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens
4856	18124		3.13	1.0E-46	AB023197.1	NT	MT-11 mRNA. (HUMAN);
6817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6098	25818	32809	5.34	1.0E-46	8923762	NT	7682501.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	26818	32810	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19902	33295	0.64	1.0E-46	BF198247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7n48e07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element
11410	24471	38136	1.61	1.0E-46	AJ245821.1	NT	MER22 repetitive element ;
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	7682501.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3943705 3'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens CTL2 gene
13176	25784		1.89	1.0E-46	AV715377.1	EST_HUMAN	802072284F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215388 5'
787	13068		3.7	9.0E-47	AJ271735.1	NT	802072284F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215388 5'
6047	18175	31152	3.05	9.0E-47	AW770528.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
6506	19672	33039	0.86	9.0E-47	11425439	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11388	24449	38110	1.4	9.0E-47	11432209	NT	h83e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009634 3' similar to TR-O75703 O75703
12874	26027	31675	1.64	9.0E-47	11417866	NT	HYPOTHETICAL 12.4 KD PROTEIN ;
1851	14997	28100	32.2	8.0E-47	Y18538.1	NT	Homo sapiens zinc finger protein ZNF288 (ZNF288), mRNA
1851	14997	28101	32.2	8.0E-47	Y18538.1	NT	Homo sapiens similar to aldo-keto reductase family 1, member B1 (aldose reductase) (H. sapiens)
2781	15897	29007	1.5	8.0E-47	5453855	NT	(LOC83083), mRNA
3089	16285	29283	2.04	8.0E-47	AJ226043.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3715	18878	29881	0.77	8.0E-47	AB041826.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3715	18878	29882	0.77	8.0E-47	AB041826.1	NT	Homo sapiens HLA-C gene, exon 6, individual 19323
12982	25822	28851	1.99	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R6E) mRNA
2013	15737	28851	3.04	6.0E-47	AL163246.2	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
9476	22333	36097	6.83	6.0E-47	AI695189.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	AV683284 GSK Homo sapiens cDNA clone GKASH11 5'
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens chromosome 21 segment HS21C046
							HSU77054 Human Homo sapiens cDNA clone NT
							1998K02.x1 NCI_CGAP_Ku111 Homo sapiens cDNA clone IMAGE:2298859 3'
							Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
							Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	19865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens GDC37 (cell division cycle 37, S. cerevisiae, homologue) (GDC37), mRNA
11035	24114		5.58	5.0E-47	M78590.1	EST_HUMAN	EST007738 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCF07
1432	14585	27660	7.03	4.0E-47	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6071	20199	33625	0.82	4.0E-47	BE93898.1	EST_HUMAN	MIR4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8677	21757	35292	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8677	21757	35293	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8618	21897	35436	0.83	4.0E-47	AW98377.1	EST_HUMAN	RCS-BN0034-220300-015-f05 BN0034 Homo sapiens cDNA
11936	24922		1.98	4.0E-47	AW615609.1	EST_HUMAN	x066607.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT8_MOUSE
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	QB4252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
558	13751	26779	2.09	3.0E-47	BE907634.1	EST_HUMAN	601467639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898721 5'
841	14019	27075	3.99	3.0E-47	N57483.1	EST_HUMAN	601467639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898721 5'
868	14141	27202	10.04	3.0E-47	AL163284.2	NT	y54604.s1 Soares_multiple_sclerosis_2NHLMSF Homo sapiens cDNA clone IMAGE:277327 3'
3376	16548	29562	0.97	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
4073	17228		6.61	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4482	17822	30603	1.14	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6136	19315	32654	4.68	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19316	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UJ-HF-BM0-adv-d-07-0-UJ11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6694	19652		1.71	3.0E-47	A122413.1	EST_HUMAN	UJ-HF-BM0-adv-d-07-0-UJ11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7540	20813	34089	0.88	3.0E-47	AB19755.1	EST_HUMAN	q104e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
9033	22112	35654	0.77	3.0E-47	AB19755.1	EST_HUMAN	WJ11H08.x1 NCI_CGAP_K1212 Homo sapiens cDNA clone IMAGE:2402558 3'
9033	22112	35655	0.77	3.0E-47	AW963796.1	EST_HUMAN	WJ11H08.x1 NCI_CGAP_J0412 Homo sapiens cDNA clone IMAGE:2402558 3'
152	19377	28409	1.21	2.0E-47	4505318	NT	EST375868 MAGC resequences, MAGH Homo sapiens cDNA
980	14162	27221	2.45	2.0E-47	AL163208.2	NT	EST375868 MAGC resequences, MAGH Homo sapiens cDNA
980	14162	27222	2.45	2.0E-47	AL163208.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1598	14751	27859	0.95	2.0E-47	AB89278.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1623	14775	27859	1.61	2.0E-47	7662109	NT	Homo sapiens chromosome 21 segment HS21C009
1712	14653	27862	4.49	2.0E-47	AA524514.1	EST_HUMAN	wq86b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478851 3'
4467	17607	30685	1.61	2.0E-47	4504868	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4503	17643	30628	1.67	2.0E-47	AA569592.1	EST_HUMAN	hg43h12.s1 NCI_CGAP_Cs3 Homo sapiens cDNA clone IMAGE:937607 3'
4503	17643	30629	1.67	2.0E-47	AA569592.1	EST_HUMAN	(Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4628	17764	30746	2.14	2.0E-47	5174648	NT	nt23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
4933	18063	31046	1.25	2.0E-47	AW985168.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
							Homo sapiens Rev/Rax activation domain binding protein-related (RAB-R) mRNA
							EST377239 MAGC resequences, MAGI Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18368		0.71	2.0E-47	A041128.1	EST_HUMAN	ov61h03.x1 Soares, testis NIH Homo sapiens cDNA clone IMAGE:1841845 3'
5804	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3867487 5'
7878	25854		1.34	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34754	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8915	21994	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9690	22739	36308	1.27	2.0E-47	11528138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	26073	31653	3.36	2.0E-47	R42423.1	EST_HUMAN	y92e08.x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:289683 3' similar to contains OFR repetitive element;
12394	26078		1.87	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
1437	14590	27663	6.42	1.0E-47	A1334420.1	EST_HUMAN	q959f03.x1 Soares, fetal lung NIH HL 19W Homo sapiens cDNA clone IMAGE:1931189 3'
3926	17095	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3926	17095	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5187	18309	31275	2.4	1.0E-47	AW813806.1	EST_HUMAN	RC3-ST0187-130400-017402 S10187 Homo sapiens cDNA
7189	20054	33464	10.76	1.0E-47	A1880886.1	EST_HUMAN	at19e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355588 3' similar to gb:M22995
8069	22148		4.24	1.0E-47	AW684648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10584	23589	37205	2.26	1.0E-47	L30115.1	NT	h84811.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1843	14795	27879	3.84	9.0E-48	AF223391.1	NT	Papio hamadryas alcohol dehydrogenase class I (ADH1) gene, 5' region
3848	16809	29823	0.73	9.0E-48	BF359947.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5797	18987	32290	1.1	9.0E-48	BE888198.1	EST_HUMAN	CN2-MT0100-310700-290-05 MT0100 Homo sapiens cDNA
5797	18987	32291	1.1	9.0E-48	BE888198.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913108 5'
6226	19401	32751	0.57	9.0E-48	A1833168.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913108 5'
6355	19525	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	at75e09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
11378	24439	36098	3.06	9.0E-48	BE338313.1	EST_HUMAN	O60844 HOMOLOG OF RAT ZMOGEN GRANULE MEMBRANE PROTEIN.;
1279	14436		1.75	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1280	14436		1.65	8.0E-48	4501800	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3205	16390	29390	5.72	8.0E-48	AW788477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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3205	16380	29391	5.72	8.0E-48	AW769477.1	EST_HUMAN	hK61B03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:364707
4041	17197	30208	0.66	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13698		2.68	7.0E-48	AB033036.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13698		18.69	7.0E-48	AB033036.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	14880	27761	1.96	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1667	14819	27902	5.39	7.0E-48	5730038	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
6685	19843	33233	24.01	7.0E-48	11416831	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
12125	25105	38809	2.98	7.0E-48	R19623.1	EST_HUMAN	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3687	16850	29658	0.88	6.0E-48	A176111.1	EST_HUMAN	y937b02.t1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:34747 5'
6183	19359	32707	0.84	8.0E-48	AB006955.1	NT	w69h03.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2388613 3'
6924	20239	33674	0.93	8.0E-48	11420995	NT	Homo sapiens mRNA for AIE-75, complete cds
7628	25849	34172	0.78	8.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25849	34173	0.78	8.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9323	22399	35953	1.57	8.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9741	22806	36382	1.87	8.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
8690	22830	36514	2.84	8.0E-48	AA189080.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
3384	18465	29586	1.48	5.0E-48	48268801	NT	zq45b06.s1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
8774	21853	35395	1.04	5.0E-48	BE084410.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
2829	15943	28053	1.02	4.0E-48	RA45715.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
11200	24269	37605	3.11	4.0E-48	AB020420.1	EST_HUMAN	He140-f Adult heart, Clontech Homo sapiens cDNA clone a140-f
12050	25031	38737	1.76	4.0E-48	BE084410.1	EST_HUMAN	bu47a02.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2254154 3'
1416	14570	27643	1.91	3.0E-48	AV690984.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
2032	15173	28282	31.61	3.0E-48	4885170	NT	AV690984 GK6 Homo sapiens cDNA clone GKGDRE12 5'
2032	15173	28283	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3505	16672	29682	0.93	3.0E-48	AF172453.1	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3721	16982	29888	0.9	3.0E-48	AW664531.1	EST_HUMAN	Homo sapiens opid growth factor receptor mRNA, complete cds
4362	17905		0.93	3.0E-48	AA009541.1	EST_HUMAN	hi14b12.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872266 3' similar to SW-DCRB_HUMAN
6015	19199	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	P66555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
7159	20232	33735	1.07	3.0E-48	AF087913.1	NT	Z04Q03.t1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:429844 5'
8585	21688		3.73	3.0E-48	AA656930.1	EST_HUMAN	MRL-BT0657-060400-201-a10 BT0657 Homo sapiens cDNA
						NT	Human endogenous retrovirus HERV-P-T47D
						EST_HUMAN	nv03f05.s1 NCI CGAP_PT22 Homo sapiens cDNA clone IMAGE:1218137 3' similar to contains PTR5.b1 PTR5 repetitive element ;

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11114	24188	37818	8.1	3.0E-48	BF514170.1	EST_HUMAN	UHH-BW1-art-e-10-Q-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
5	13244	26245	0.66	2.0E-48	AA465007.1	EST_HUMAN	z60c03.1 Scores ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:810052 5'
46	13285	26294	1.7	2.0E-48	AA631940.1	EST_HUMAN	frnfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4654	17790	30774	0.99	2.0E-48	BE240085.1	EST_HUMAN	TCSAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCSA Homo sapiens cDNA clone TCSAP3842
5935	19121	32433	0.84	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
5935	19121	32434	0.84	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
7688	20753	34236	3.98	2.0E-48	AB040334.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7688	20763	34237	3.99	2.0E-48	AB040334.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7703	20768	34253	3.84	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8550	21631	35168	1.13	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
12109	25089		1.36	2.0E-48	AW291799.1	EST_HUMAN	UI-H-B12-egl-b-11-Q-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724453 3'
12320	13244	26245	2.98	2.0E-48	AA465007.1	EST_HUMAN	z60c03.1 Scores ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:810052 5'
12674	25990	31771	1.25	2.0E-48	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
57	13295	26311	2.33	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
896	14072	27137	4.67	1.0E-48	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein (APP)), mRNA
1101	14266	27323	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1101	14268	27324	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1324	14481	27548	4.01	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1968	15111	28212	13.8	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3577	16742	29759	0.94	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5240	18382	31330	1.1	1.0E-48	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6417	19596	32948	1.24	1.0E-48	AJ889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR-O14588 O14588 SIMILARITY TO U73941
6417	19596	32949	1.24	1.0E-48	AJ889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR-O14588 O14588 SIMILARITY TO U73941
6628	19788		0.87	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6727	19883	33274	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6727	19883	33275	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7407	20485	33954	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9031	22110	35651	0.65	1.0E-48	4759695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9031	22110	35652	0.65	1.0E-48	4759695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA

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9414	22488	36053	0.99	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9468	22625	36088	6.78	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9781	22821	36398	4.74	1.0E-48	BF304683.1	EST_HUMAN	80188808F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 6'
10581	23816	37221	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10581	23816	37222	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12282	26014		1.41	1.0E-48	W26785.1	EST_HUMAN	15d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2064	15204	28320	0.97	8.0E-49	AB026497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
6178	19354	32701	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6178	19354	32702	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8491	21572	35109	3.09	8.0E-49	U23850.1	NT	Homo sapiens gene for activin receptor type 1B, complete cds
10194	23231	96822	0.93	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type 1B, complete cds
11098	24169	97804	3.65	8.0E-49	AB22722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element
12097	25077	38785	2.08	8.0E-49	AA872183.1	EST_HUMAN	cb78a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1837462 3'
142	13602	26637	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
142	13602	26638	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26637	1.82	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26638	1.82	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26637	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26638	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1248	14407	27459	4.37	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4772	17907	30890	0.9	7.0E-49	CG0811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845Q24.3
5578	18771	31815	2.33	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54823
5586	18781	31828	1.3	7.0E-49	AL120937.1	EST_HUMAN	O54823 RSEC15.1
5926	18771	31815	0.78	7.0E-49	AI807191.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762C033 3'
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54823
							O54823 RSEC15.1
							bc55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:U17208 40S
							RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
202	13425	26456	20.33	6.0E-49	AW731740.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: harny2) Homo sapiens cDNA clone DKFZp761A138 3'
4231	17378	30387	0.84	6.0E-49	AL162091.1	EST_HUMAN	h444602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O96636
5954	19140	32458	0.84	6.0E-49	AW511225.1	EST_HUMAN	O96636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.1
6572	19734	33113	1.27	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'

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11557	24812	38291	3.39	6.0E-49	AW452218.1	EST_HUMAN	UHH-B13-alo-a-05-OJL.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11961	24946	38650	2.48	6.0E-49	AA386556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
11961	24946	38651	2.48	6.0E-49	AA386556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
12670	25897		10.54	6.0E-49	AA707667.1	EST_HUMAN	z29cd08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
730	13912	26951	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26952	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1838	14983	28082	10.18	6.0E-49	AA172121.1	EST_HUMAN	z29cd07.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to
2808	15922	28032	7.1	5.0E-49	U17714.1	NT	TR:G233228 G233228 RTV-H PROTEIN, contains LTR7.13 LTR7 repetitive element ;
3348	18519	29533	7.58	5.0E-49		NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
538	19791	28754	28.38	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC63362), mRNA
7395	20473	33939	0.96	4.0E-49	Z26634.2	NT	X08607.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875583 3' similar to WP:B0350.2B
7395	20473	33940	0.96	4.0E-49	Z26634.2	NT	CE06703 ;
7422	20489	33970	0.88	4.0E-49	11525737	NT	Homo sapiens mRNA for ankryrin B (440 kDa)
7422	20489	33971	0.88	4.0E-49	11525737	NT	Homo sapiens mRNA for ankryrin B (440 kDa)
7992	21042	34554	0.89	4.0E-49	7662209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 8
9065	22144	35690	0.47	4.0E-49	11425374	NT	(GalNAc-T8) (GALNT8), mRNA
9065	22144	35691	0.47	4.0E-49	11425374	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 8
12514	26145		2.74	4.0E-49	AA210798.1	EST_HUMAN	(GalNAc-T8) (GALNT8), mRNA
12615	25413		2.93	4.0E-49	AF240788.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
574	13798	26789	0.91	3.0E-49	X68968.1	NT	Homo sapiens copine III (CPNE3), mRNA
2713	15831		2.73	3.0E-49	AA016131.1	EST_HUMAN	Homo sapiens copine III (CPNE3), mRNA
5098	18228	31198	2.68	3.0E-49	U46899.1	NT	z80705.r1 NCJ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:682977 5'
7577	20649	34127	0.83	3.0E-49	H39479.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11582	24636	38316	1.41	3.0E-49	AA387661.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
678	13894		1.93	2.0E-49	BE165980.1	EST_HUMAN	z831c05.r1 Soares retina N2b-4-IR Homo sapiens cDNA clone IMAGE:380584 5' similar to contains L1.13 L1
3294	16483	29487	1.15	2.0E-49	N26448.1	EST_HUMAN	repetitive element ;
							Human type IV collagen (COL4A6) gene, exon 40
							EST25612 WATM1 Homo sapiens cDNA clone 25e12
							EST42572 Endometrial tumor Homo sapiens cDNA 5' end
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
							y23cd06.r1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:262571 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	18822	28832	0.86	2.0E-49	AF028564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6876	20027	33437	1.2	2.0E-49	AV717088.1	EST_HUMAN	AV717088 DCB Homo sapiens cDNA clone DCB1B01 5'
8291	21373		1.87	2.0E-49	M86033.1	EST_HUMAN	EST025588 Fetal brain, Stratiogene (cat#9636208) Homo sapiens cDNA clone HFBCY60
12626	26008		2.69	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	14097		9.1	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862086 5'
1584	14738	27816	73.58	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1844	14990	28091	2.93	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3366273 5'
5476	18074	31989	4.68	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6202	19377	32728	0.85	1.0E-49	H16291.1	EST_HUMAN	Yr48h04.r1 Soares adult brain N2b5H1855Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN (GT) GAMMA-1 SUBUNIT ;
6208	19883	32793	1.09	1.0E-49	AW984940.1	EST_HUMAN	EST376713 IMAGE resequences, MAGH Homo sapiens cDNA
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3620863 5'
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7453	20530	34003	2.09	1.0E-49	N25884.1	EST_HUMAN	Yw78g12.s1 Soares placenta_8109weeks_2NbhHP8109W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7453	20530	34004	2.09	1.0E-49	N25884.1	EST_HUMAN	Yw78g12.s1 Soares placenta_8109weeks_2NbhHP8109W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8874	21953		0.71	1.0E-49	9994184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120). mRNA
9183	22271	36809	1.48	1.0E-49	BE468340.1	EST_HUMAN	601300982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10331	23366	36975	1.23	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423.J1 434 (synonym: h1853) Homo sapiens cDNA clone DKFZp434D2423 5'
11304	24369	38010	1.32	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDRAWED4 5'
11580	24843	38326	2.91	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12148	25119		1.28	1.0E-49	BE168343.1	EST_HUMAN	MRO-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
12508	25349		1.82	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5109	18237		0.92	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
6834	26215		0.63	9.0E-50	BE268758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
174	13398	26426	4.18	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
737	13919	26959	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
737	13919	26960	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1803	14982	28049	4.32	8.0E-50	4601890	NT	Homo sapiens actinin, alpha 1 (ACTN1), mRNA
2552	15677	28900	1.05	8.0E-50	7705394	NT	Homo sapiens p47 (LOC51674), mRNA
2552	15677	28801	1.05	8.0E-50	7705394	NT	Homo sapiens p47 (LOC51674), mRNA
2764	15879	28988	2.42	8.0E-50	4828658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
2881	15160		2.67	8.0E-50	D80334.1	NT	Homo sapiens hepatocyte growth factor (HGF) gene, exon 18

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
634	13819	26843	1.07	7.0E-50	BE088591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6923	20238	33672	0.73	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6923	20238	33673	0.73	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7457	20533	34008	0.74	7.0E-50	AA627822.1	EST_HUMAN	mq6a12.e1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X63391.60S
10993	24072	37705	23.18	7.0E-50	AB72137.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
4482	17602		0.67	6.0E-50	BE794381.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439008 3'
8408	21489		3.28	6.0E-50	BE044076.1	EST_HUMAN	60158665F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843577 6'
11053	24130	37765	3.32	6.0E-50	AA312079.1	EST_HUMAN	h038104.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29.b3
11053	24130	37766	3.32	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element;
1835	14982	28080	1.34	5.0E-50	BF332638.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1835	14982	28081	1.34	5.0E-50	BF332638.1	EST_HUMAN	EST182776 Jurkat T-cells VI Homo sapiens cDNA 5' end
9284	22370		5.27	5.0E-50	AA557683.1	EST_HUMAN	CMA0-BT0792-300500-388-b05 BT0792 Homo sapiens cDNA
12080	28070	38777	1.78	5.0E-50	AA403053.1	EST_HUMAN	CMA0-BT0792-300500-388-b05 BT0792 Homo sapiens cDNA
940	14114		2.91	4.0E-50	AA801143.1	EST_HUMAN	nl45h10.e1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043083 similar to contains PTR5.13 PTR5
3336	16701	29712	2.08	4.0E-50	AL163248.2	NT	repetitive element;
6491	19557	33020	0.92	4.0E-50		NT	z182b01.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
7383	20481	33824	1.02	4.0E-50	BE087538.1	EST_HUMAN	G1335769 GAG-POL POLYPEPTIDE ;
1982	15194		9.4	3.0E-50	M18048.1	NT	no54609.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
3371	16543	29557	0.92	3.0E-50	AA746142.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3846	17006	30008	0.9	3.0E-50	AW75254.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
6815	19388	33374	0.89	3.0E-50	11416817	NT	Homo sapiens cystathionine synthetase (CARS), mRNA
6815	19388	33375	0.89	3.0E-50	11416817	NT	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
6804	20219	33649	1.71	3.0E-50		NT	Human endogenous retrovirus RTVL-H2
7822	20877	34376	5	3.0E-50	AF233436.2	NT	cd03308.s1 NCI_CGAP_K13 Homo sapiens cDNA clone IMAGE:1322627 3'
7822	20877	34377	5	3.0E-50	AF233436.2	NT	QV1A5 Homo sapiens cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
							Cardiomyopathy associated gene 5
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens similar to semaphorin domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP-1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP-1a mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8782	21861	35404	0.68	3.0E-50	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	23061	36657	1.08	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10032	23070	36670	1.03	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10737	23770	37380	1.04	3.0E-50	AB002297.1	NT	Homo sapiens mRNA for KIAA0299 gene, partial cds
11364	24425	38080	1.51	3.0E-50	11436955	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
11752	23938	37564	8.19	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
13217	25782	31822	1.35	3.0E-50	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
789	13978		7.84	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1104	14269	27327	6.16	2.0E-50	4557752	NT	Homo sapiens midline 1 (Optic/BBB syndrome) (MID1) mRNA
1474	14827	27713	33.77	2.0E-50	AF198303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4376	17519	30498	0.75	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
5329	18442	31412	1.37	2.0E-50	AB016319.1	NT	Homo sapiens mRNA for KIAA0776 protein, partial cds
7007	20143	33562	0.61	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001608 5'
8511	21592	35126	1.03	2.0E-50	AB033162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8511	21592	35127	1.03	2.0E-50	AB033162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8650	21730	35288	7.21	2.0E-50	X06958.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8650	21730	35289	7.21	2.0E-50	X06958.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10088	23128	36728	1.8	2.0E-50		NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
10088	23128	36729	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11960	24945		1.39	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
474	13069	26701	2.17	1.0E-50	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2438	15566		10.11	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10386	23431	37038	1.65	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6104	19284	32817	1.04	9.0E-51	AW511225.1	EST_HUMAN	h444602.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR:065636
6354	19324	32881	0.58	9.0E-51	AA744837.1	EST_HUMAN	O65636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
8872	21951	35487	0.7	9.0E-51	AJ791154.1	EST_HUMAN	h473603.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9525	22990	36161	1.29	9.0E-51	AA043793.1	EST_HUMAN	ab23504.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
9700	22749	36317	0.68	9.0E-51	AJ791154.1	EST_HUMAN	SW_PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9700	22749	36318	0.68	9.0E-51	AJ791154.1	EST_HUMAN	ab23504.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:466362 5'
11764	23950	37579	1.97	9.0E-51	H88078.1	EST_HUMAN	SW_PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							ab23504.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
							SW_PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							jw24g06.r1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:283210 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11764	23950	37580	1.97	9.0E-51	H83078.1	EST_HUMAN	yw24g06.t1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
12068	25050	38768	1.84	9.0E-51	AA885514.1	EST_HUMAN	am10h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488451 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE ;
4558	17697	30677	1.11	8.0E-51	4503832	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4559	17697	30678	1.11	8.0E-51	4503832	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4690	17825	30812	5.38	8.0E-51	AA610942.1	EST_HUMAN	np88g09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gbX12871_mn1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7321	20403	33865	0.71	8.0E-51	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
7830	20895	34387	2.11	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
8664	22626	34987	1.05	8.0E-51	AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3354	16528	29541	1.27	7.0E-51	AW888219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3447	16815	29633	0.82	7.0E-51	AW274720.1	EST_HUMAN	xa34a03.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TRC82340
4282	17427	30416	1.37	7.0E-51	AL078628.1	EST_HUMAN	Q82340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4282	17427	30417	1.37	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2229_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4375	17518	30498	1.18	7.0E-51	11421995	NT	DKFZp434B2229_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4471	17611	30588	1.44	7.0E-51	AW285603.1	EST_HUMAN	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
11895	24970	36674	1.36	7.0E-51	AF161448.1	NT	UJ-H-81W0-elp-b-05-QJ1.s1 NCI_CGAP_Sub86 Homo sapiens cDNA clone IMAGE:2729817 3'
1557	14710	27790	0.94	6.0E-51	6878763	NT	Homo sapiens HSPC331 mRNA, partial cds
						NT	Homo sapiens putative DNA binding protein (M98), mRNA
2036	15177	28267	5.83	6.0E-51	7657288	NT	Homo sapiens KIAA0928 protein Misc2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
3582	16727	28743	14.85	6.0E-51	7657288	NT	Homo sapiens KIAA0928 protein Misc2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
4426	17588	30547	0.66	6.0E-51	6910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 8 (SLC2A8), mRNA
4426	17588	30548	0.66	6.0E-51	6910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 8 (SLC2A8), mRNA
6113	19293	32628	1.48	6.0E-51	X01788.1	NT	Human heparin-binding related (Hpr) gene exon 3
6124	19303	32642	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6124	19303	32643	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6800	20215	33845	0.93	6.0E-51	4506738	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7032	20168	33590	0.82	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC66800), mRNA
7104	18531	31486	2.15	6.0E-51	11426566	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
9337	22413	35985	0.69	6.0E-51	11426525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9337	22413	35986	0.69	6.0E-51	11426525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9885	22925	36509	2.05	6.0E-51	7681535	NT	Homo sapiens B9 protein (B9), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9964	23003	36508	0.79	6.0E-51	U50083.1	NT	Human ankyrin (ANK1) gene, exon 2
11534	24590	38265	1.84	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
814	13983	27047	6.22	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
828	14004	27061	1.71	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1015	18028	27247	2.39	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1638	14780	27875	1.14	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2658	15781	28894	10.38	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
4055	17211	30221	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4055	17211	30222	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5183	18305	31269	1.04	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11558	24813	38262	3.8	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
137	13363	26387	14.26	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
1203	14365	27425	48.14	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1976	15119	28220	1.38	3.0E-51	AA211288.1	EST_HUMAN	tr81c09.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
4446	17586	30587	1.85	3.0E-51	AL158142.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							2q87g01.s1 Stragene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:649008 3'
							Novel human gene mapping to chromosome 22
7753	20813	34304	2.3	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:63233 5' similar to gb:M14123_cde4
9040	22119		3.85	3.0E-51	M29063.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
9268	26227		0.61	3.0E-51	AW58377.1	EST_HUMAN	Human hnRNP C2 protein mRNA
12887	25578		6.56	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
377	13585	28619	1.88	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
706	13689	26921	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
708	13689	26922	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1723	14873	27865	16.76	2.0E-51	AA233352.1	EST_HUMAN	2730a05.J1 Stragene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN, contains LTR7.13 LTR7 repetitive element;
3927	16867	29990	3.05	2.0E-51	AI462416.1	EST_HUMAN	927g03.x1 NCI CGAP Kld11 Homo sapiens cDNA clone IMAGE:2713732 3'
4816	17753	30734	1.21	2.0E-51	AW137826.1	EST_HUMAN	UIH-BI1-adj-4-02-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
6326	18439	31408	0.66	2.0E-51	AI381520.1	EST_HUMAN	tr76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2062622 3' similar to TR:P63107 P63107 PF20.1

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6139	19317	32658	3.54	2.0E-51	BE782015.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7462	20537		0.73	2.0E-51	AF215927.1	NT	Homo sapiens diacylglycerol kinase Iota (DGKI) gene, exon 23
7615	20685	34161	1.29	2.0E-51	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0088), mRNA
8896	21975	35512	1.61	2.0E-51	BE901694.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8898	21975	35513	1.61	2.0E-51	BE901694.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9235	22312	35854	1.03	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9712	22777	36347	1.76	2.0E-51	AB17078.1	EST_HUMAN	1574407.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9803	22843	36420	4.86	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9818	22858	38438	0.69	2.0E-51	AB007928.1	NT	MF3-HTD487-150200-113-901 HTD487 Homo sapiens cDNA
10648	23682	37293	1.58	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10690	23723	37328	1.07	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	EST91298 Synovial sarcoma Homo sapiens cDNA 5' end
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	083409.x5 NCI_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1325608 3' similar to SW:NME1_MOUSE
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	083409.x6 NCI_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1325608 3' similar to SW:NME1_MOUSE
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11610	18762	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) homolog; translocated to, 4
12880	25571	31882	1.62	2.0E-51	11419159	NT	(MILLT4), mRNA
117	13348	26375	10.94	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1523	14678		37.16	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
4918	18048	31036	0.82	1.0E-51	AF111768.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
5505	18704	31720	3.7	1.0E-51	T18882.1	EST_HUMAN	b12058 Testis 1 Homo sapiens cDNA clone b12058
7827	20882	34384	1.03	1.0E-51	AI572532.1	EST_HUMAN	1639502.x1 Soares_NIHMFU_S1 Homo sapiens cDNA clone IMAGE:2089108 3'
8037	21169	34884	0.51	1.0E-51	BF434359.1	EST_HUMAN	768602.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3844081 3' similar to TR:P87892 P87892
12076	26232		1.97	1.0E-51	AV760590.1	EST_HUMAN	PROTEASE ;
12610	25409		9.43	9.0E-52	AA777621.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB802 5'
156	13381	28412	11.42	8.0E-52	AA720574.1	EST_HUMAN	285407.s1 Soares_fetal_liver_spleen_1NF.LS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
1526	14679	27760	2.39	8.0E-52	XB4900.1	NT	contains THR13 THR repetitive element ;
1689	14838	27922	2.85	8.0E-52	11986028	NT	11921 g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
							THR repetitive element ;
							H.sapiens mRNA for laminin-5, alpha3b chain
							Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14838	27923	2.85	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27922	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27923	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7688	20751	34232	0.76	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7688	20751	34233	0.76	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9215	22293	35838	1.86	7.0E-52	W96471.1	EST_HUMAN	cd59a08.1 Scores_parallel_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1214	14375		0.63	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271209-049-d07 BT0537 Homo sapiens cDNA
1729	14878	27870	7.1	6.0E-52	AF106907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5945	19035	32341	1.05	6.0E-52	AI208794.1	EST_HUMAN	9844f04.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11484	24543	38214	2.36	6.0E-52	BE048172.1	EST_HUMAN	tz48h04.y1 NCI CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW-PCGM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
4562	17700	30882	2.27	6.0E-52	Z78888.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pa18H7
9592	22947	39218	0.48	6.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1805	14847	27931	1.66	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1829	14877	28072	1.63	4.0E-52	4758843	NT	Homo sapiens nucleoporin 158kD (NUP155) mRNA
4037	17183	30203	0.77	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4882	17995	30980	0.81	4.0E-52	AI768814.1	EST_HUMAN	w88b502.x1 NCI CGAP_JGd12 Homo sapiens cDNA clone IMAGE:2400459 3'
5401	18503	31574	1.3	4.0E-52	4508132	NT	Homo sapiens phosphatidylyl pyrophosphate synthetase-associated protein 2 (PRP-SAP2) mRNA
5401	18503	31575	1.3	4.0E-52	4508132	NT	Homo sapiens phosphatidylyl pyrophosphate synthetase-associated protein 2 (PRP-SAP2) mRNA
8228	21310	34830	1.18	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8731	21811	35347	5.5	4.0E-52	11417035	NT	Homo sapiens hydrocortisoid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12429	25304		3.44	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12867	25042		12.78	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13141	25741		1.3	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4204	17353		11.41	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
576	13768	26780	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
576	13768	26781	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2071	15211	28328	1.18	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2568	15693	28818	1.5	2.0E-52	BE207575.1	EST_HUMAN	b68607.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2768	15011		11.46	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:4248891 5'
5092	18220	31190	3.41	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5128	18251	31216	1.4	2.0E-52	AI141802.1	EST_HUMAN	qs5605.s1 Soares_NHr-MPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5128	18251	31217	1.4	2.0E-52	AI141802.1	EST_HUMAN	qs5605.s1 Soares_NHr-MPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
6821	19011	32317	3.24	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-063-E12 CT0214 Homo sapiens cDNA
6497	19863	33026	1.98	2.0E-52	11141868	NT	Homo sapiens Interleukin 21 receptor (IL21R), mRNA
6853	20006	33415	0.86	2.0E-52	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7081	20175	33597	0.76	2.0E-52	AI782146.1	EST_HUMAN	oa45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
7996	21046	34558	0.69	2.0E-52	6032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
7996	21046	34559	0.69	2.0E-52	6032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8854	21933		8.71	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9196	22215	35759	0.96	2.0E-52	AA778795.1	EST_HUMAN	z445g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15KD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
9690	22842		1	2.0E-52	4758789	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36965	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36968	4.8	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11481	24540	38209	3.14	2.0E-52	AI931462.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
11481	24540	38210	3.14	2.0E-52	AI931462.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
11491	24550	38225	2.52	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCB.AE03 5'
11634	24714		1.46	2.0E-52	W70260.1	EST_HUMAN	z149g12.f1 Soares_fetal_heart_Nhr-H19W Homo sapiens cDNA clone IMAGE:344038 5'
11918	24804		3.25	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12234	26194	31541	5.9	2.0E-52	AW236297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element ;
12658	26437		5.72	2.0E-52	AI806985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_C9C_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TRC18659
548	13739	26764	1.89	1.0E-52	AA634445.1	EST_HUMAN	Q16859 CARBOXYLESTERASE ;
1402	14856	27630	18.76	1.0E-52	4504026	NT	z175h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743878 3'
2600	15724		1.88	1.0E-52	4502238	NT	Homo sapiens glutamate-aminomethylase (glutamine synthase) (GLUL) mRNA
							Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
							pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
3126	16302	29315	2.6	1.0E-52	SG1070.1	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18648	31626	4.43	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6523	18888	33082	2.33	1.0E-52	U38964.1	NT	Human PMS2 related (PMSR2) gene, complete cds
7388	20659	34135	2.07	1.0E-52	X07282.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8014	21064	34576	0.59	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (hnp) and survival motor neuron protein (smn) genes, complete cds
8660	21740		1.18	1.0E-52	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9390	22465	36029	0.77	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10804	23837		0.68	1.0E-52	AW020370.1	EST_HUMAN	af0805.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483146 5'
10914	23947		1.08	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11004	24083	37720	2.12	1.0E-52	U48286.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (PTPCAAX1) mRNA, complete cds
11075	24150		1.72	1.0E-52	11428321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
12135	25116	38819	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
12135	25115	38820	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3891	17050	30049	0.69	9.0E-53	4508084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4611	17660	30638	3.3	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12480	25532		6.65	7.0E-53	BF238465.1	EST_HUMAN	601804771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4192786 5'
12958	26046		7.06	7.0E-53	AA421782.1	EST_HUMAN	644807.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2069077 3' similar to contains THR.11 THR repetitive element:
4214	17363	30351	4.46	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
5283	18411	31377	0.92	5.0E-53	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12528	25360		1.93	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-161090-011-g 10 ST0197 Homo sapiens cDNA
50	13289	26301	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
50	13289	26302	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9816	22671		0.87	4.0E-53	A1613037.1	EST_HUMAN	cy06h04.x1 NCI_CGAP_UJ3 Homo sapiens cDNA clone IMAGE:2278327 3'
9958	22987		0.94	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11489	24548	38221	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810698F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4063977 5'
11489	24548	38222	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810698F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4063977 5'
2726	15944	28955	2.94	3.0E-53	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL4 genes, complete cds)
3825	16955	29988	1.18	3.0E-53	AW060836.1	EST_HUMAN	wr22x207.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2568798 3'
4713	17848	30831	0.75	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-056-D03 UM0081 Homo sapiens cDNA
5541	18738	31755	0.97	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 8 mRNA, complete cds
5743	18938	32238	1.01	3.0E-53	11528287	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6323	19495	32851	1.46	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7247	20330	33776	0.76	3.0E-53	Y10388.3	NT	H.septens graef gene
7247	20330	33777	0.76	3.0E-53	Y10388.3	NT	H.septens graef gene
8469	21580	35116	10.97	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9060	22139	35683	0.85	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP-5), mRNA
9257	22334		9.77	3.0E-53	5901853	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
12361	25259		1.18	3.0E-53	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
470	19665		11.25	2.0E-53	AA366556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
2068	16209	28325	3.29	2.0E-53	7705394	NT	Homo sapiens hyaluronic acid receptor (HAR), mRNA
2404	15535	28682	0.28	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds
2601	15725		12.68	2.0E-53	4502310	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3290	18484	29483	0.79	2.0E-53	7705887	NT	Homo sapiens leucine aminopeptidase (LOC51058), mRNA
3317	18490	29508	1.28	2.0E-53	AF093822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 8
4170	17320	30313	2.99	2.0E-53	MB1873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
5542	18739	31756	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT03098-170800-001-g03 CT0398 Homo sapiens cDNA
5542	18739	31757	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT03098-170800-001-g03 CT0398 Homo sapiens cDNA
8055	21138	34658	1.01	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
8196	21278		0.48	2.0E-53	AA095652.1	EST_HUMAN	15428 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9608	22663		3.47	2.0E-53	AW245676.1	EST_HUMAN	2822665.5prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822665 5'
10882	23895	37517	0.59	2.0E-53	BE550195.1	EST_HUMAN	7650602.1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04008 Q04009 MYOSIN HEAVY CHAIN.;
1477	14630	27715	2.2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3496	16963	28675	2.99	1.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5078	18206	31178	1.06	1.0E-53	BE296386.1	EST_HUMAN	601176725F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3531919 5'
6831	19984	33392	1.5	1.0E-53	BF368420.1	EST_HUMAN	GM4-N1029-150800-543-e02 NN1028 Homo sapiens cDNA
7397	20475	33942	0.87	1.0E-53	BE12071.1	EST_HUMAN	RC6-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8120	21202	34723	0.6	1.0E-53	AA249072.1	EST_HUMAN	19571 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9260	22368	35915	4.73	1.0E-53	X78536.1	NT	H.septens mRNA for hnRNPcore protein A1
12228	25178	38345	1.47	1.0E-53	AW245422.1	EST_HUMAN	2822943.3prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822943 5'
3324	16497	29515	0.61	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5417	25803	31593	5.86	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
212	13435	26465	1.29	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC.20 Homo sapiens cDNA clone IMAGE:3614031 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1882	15028	28133	2.08	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6057	19239	32564	23.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
395	19632	26669	1.35	7.0E-54	AA812537.1	EST_HUMAN	at79c12.s1 Soares_basalis_NHT Homo sapiens cDNA clone 1377040 3' similar to contains MER30.13 MER30
1877	15021	28128	2.23	7.0E-54	Y16645.1	NT	repetitive element ;
2278	15410	28541	7.63	7.0E-54	N27177.1	EST_HUMAN	Homo sapiens mRNA for monocyte chemotactic protein-2
10333	23368	36978	2.1	7.0E-54	11417222	NT	yw68d12.s1 Soares_placenta_8to9weeks_2NtHP8to9W Homo sapiens cDNA clone IMAGE:257389 3' similar to contains LTR7.b3 LTR7 repetitive element ;
11365	24426	38081	1.4	7.0E-54	8923698	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
11365	24426	38082	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11570	24825		3.42	7.0E-54	AI160189.1	EST_HUMAN	Homo sapiens golgin-like protein (GLP), mRNA
25	13263	26295	0.84	6.0E-54	AB003618.1	NT	qb87g03.x1 Soares_fetal_heart_Nbt-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.t1 ORF repetitive element ;
396	13633	28670	0.77	6.0E-54	8922148	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
396	13633	28671	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3365	16527	28542	0.72	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4111	17265	30285	22.75	6.0E-54	4502872	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4584	17721	30704	1.09	6.0E-54	AV754746.1	EST_HUMAN	Homo sapiens chloride channel 6 (CLCN6) mRNA
4968	18097	31079	2.15	6.0E-54	4505806	NT	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4998	18125		2.04	6.0E-54	Y09846.1	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
6115	18125		3.31	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
11741	23927	37552	1.52	6.0E-54	AW813567.1	EST_HUMAN	H. sapiens shc pseudogene, p66 isoform
2218	15352	28483	1.94	6.0E-54	P51523	SWISSPROT	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA
187	13409		56.19	4.0E-54	AF110103.1	NT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
978	14151	27211	14.58	4.0E-54	AA306784.1	EST_HUMAN	Tupala belangeri beta-actin mRNA, partial cds
1848	14894	28096	3.26	4.0E-54	D38521.1	NT	EST1177698 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1948	14894	28097	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3274	16448		1.85	4.0E-54	AI95098.1	EST_HUMAN	Human mRNA for KIAA0077 gene, partial cds
96	13331	28358	8.12	3.0E-54	AA313487.1	EST_HUMAN	wc26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328269 3' similar to TR:O02711
1604	14757		0.96	3.0E-54	AW615742.1	EST_HUMAN	O02711 PRO-POL-OUTPASE POLYPROTEIN ;
2635	15758	28872	1.19	3.0E-54	AL110383.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							td87g08.x1 NCI_OGAP_GC8 Homo sapiens cDNA clone IMAGE:2816542 3'
							DKFZp434E0731_1 434 (synonym: hscd) Homo sapiens cDNA clone DKFZp434E0731 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6024	19207	32527	1.36	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7548	20620	34098	1.34	3.0E-54	AA844081.1	EST_HUMAN	ai52c08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7548	20620	34097	1.34	3.0E-54	AA844081.1	EST_HUMAN	ai52c08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
11277	24344		1.77	3.0E-54	11434808	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11341	24404	38053	4.01	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NC1 CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155121 5'
11650	24729	38421	2.88	3.0E-54	AA393382.1	EST_HUMAN	z170f12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR-G101315
12338	25243	32110	1.32	3.0E-54	AW095459.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
12379	26149		3.18	3.0E-54	AW748955.1	EST_HUMAN	EST368828 MAGE resequences, MAGEC Homo sapiens cDNA
659	13845	26871	17.97	2.0E-54	5031900	NT	RC1-BT0313-131189-011-609 BT0313 Homo sapiens cDNA
1396	14550	27825	1.54	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
2604	15727	28846	1.25	2.0E-54	AW163175.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2656	15787	28903	2.25	2.0E-54	AL163210.2	NT	ai82p03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13016 GULLIN HOMOLOG 1;
2660	16137	28155	1.95	2.0E-54	AW057924.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3392	16862	28577	0.8	2.0E-54	AJ278314.1	NT	WV60b12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING;
3638	16802		6.1	2.0E-54	AA532825.1	EST_HUMAN	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
4321	17484		1.74	2.0E-54	4502642	NT	nt45g09.s1 NC1 CGAP_P19 Homo sapiens cDNA clone IMAGE:985488 similar to gb:X53777 80S
4563	17701		7.1	2.0E-54	AF208161.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5591	18786	31833	2.66	2.0E-54	4758069	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
5720	18913	32209	1.21	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
5882	18071	32379	3.99	2.0E-54	11428657	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5982	19167	32487	11.29	2.0E-54	AB046811.1	NT	tz43c11.y1 NC1 CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291348 5'
5982	19167	32488	11.29	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6796	19951	33351	1.63	2.0E-54	AF006915.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
6950	20263	33701	0.68	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6950	20263	33702	0.68	2.0E-54	AB023212.1	NT	Homo sapiens EV15 homolog mRNA, complete cds
7273	20356	33810	8.33	2.0E-54	11428544	NT	Homo sapiens mRNA for KIAA0935 protein, partial cds
8828	22869	36451	3.98	2.0E-54	AB001025.1	NT	Homo sapiens neurofibronin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
10213	23249	36838	1.14	2.0E-54	11429127	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
10326	23361	36871	0.76	2.0E-54	11416762	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
							Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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10326	23361	36872	0.76	2.0E-54	11418762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10841	23874	37494	0.46	2.0E-54	AB007831.1	NT	Homo sapiens mRNA for KIAA0462 protein, partial cds
11275	19851	33351	1.46	2.0E-54	AF008916.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
12027	25011		1.72	2.0E-54	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
12893	25591	31970	4.38	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4587	17724		1.65	1.0E-54	BF315418.1	EST_HUMAN	601888230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8927	22006	35545	0.5	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
10459	23494	37105	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10609.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'
10459	23494	37106	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10609.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'
13086	25709		2.33	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10588	23603	37208	1.02	9.0E-55	BE081469.1	EST_HUMAN	QV2-B10G35-160400-143-h12 B10G35 Homo sapiens cDNA
1344	14500		1.59	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1348	14503		2.77	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11471	24530		1.83	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860907 5'
9004	22083		0.48	7.0E-55	AW103839.1	EST_HUMAN	xd78-c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2803522 3' similar to TR:060365
9383	22458	36021	1.28	7.0E-55	AA893581.1	EST_HUMAN	O60365 FOS39554_1.;
9416	22490	36055	1.71	7.0E-55	AU139309.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
11485	24544	38215	8.08	7.0E-55	AI561050.1	EST_HUMAN	AU139309 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11485	24544	38216	8.08	7.0E-55	AI561050.1	EST_HUMAN	tg29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
12726	25911	31860	1.18	7.0E-55	BE670608.1	EST_HUMAN	tg29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
13050	28063		6.37	7.0E-55	H23399.1	EST_HUMAN	7637c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284940 3'
11804	24794	38492	1.98	6.0E-55	AB040334.1	NT	ym5/g07.t1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
1810	14959	28051	1.21	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
1810	14959	28052	1.21	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
4894	18024	31010	1.51	5.0E-55	AW206021.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6670	19829	33217	1.49	5.0E-55	4502240	NT	UJH-B11-efy-g-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2725356 3'
6670	19829	33218	1.49	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6805	25833	33360	1.08	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6805	25833	33361	1.08	5.0E-55	4505952	NT	Homo sapiens paracetamolase 2 (PON2) mRNA, and translated products
7182	20314	33757	1.03	5.0E-55	7382477	NT	Homo sapiens paracetamolase 2 (PON2) mRNA, and translated products
7446	20523	33986	0.72	5.0E-55	11434422	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA

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9244	22321	36986	2.3	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9520	22585		0.91	5.0E-55	BE064388.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
10243	23278	36872	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10243	23278	36873	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10427	23462	37089	1.13	5.0E-55	5453765	NT	Homo sapiens nrl (chicken)-like 2 (NEL2), mRNA
11502	24580	38238	1.3	5.0E-55	11421849	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
11502	24580	38237	1.3	5.0E-55	11421849	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
12421	25298		1.73	5.0E-55	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
56	18004	26310	2.24	4.0E-55	AW957994.1	EST_HUMAN	EST370084 MAGe resequences, MAGe Homo sapiens cDNA
689	13873	26906	32.17	4.0E-55	4828973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1472	14626	27710	2.15	4.0E-55	7861713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1472	14626	27711	2.15	4.0E-55	7861713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1544	14896		1.72	4.0E-55	BF061411.1	EST_HUMAN	Homo sapiens predicted osteoblast protein (GS3786), mRNA
2081	15221	28341	2.19	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2081	15221	28342	2.19	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2151	15287	28412	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2151	15287	28413	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2384	15515	28844	3.02	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8539	21620		9.85	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11605	24563		2.31	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12937	25244		1.82	4.0E-55	BF303941.1	EST_HUMAN	60186575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8731	19887	33279	0.88	3.0E-55	AA077166.1	EST_HUMAN	7808A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B08A09
12273	25205		4.18	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-060300-001-g08 HT0603 Homo sapiens cDNA
13103	25719		3.53	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
388	13594	26630	1.69	2.0E-55	X57147.1	NT	Human endogenous retrovirus pH-E.1 (ERV9)
565	13757		1.09	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
666	13852	26880	3.98	2.0E-55	4507298	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
3023	16199	29222	0.89	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4897	18027	31014	3.51	2.0E-55	BE19888.1	EST_HUMAN	GM1-HT0878-150800-357-g03 HT0878 Homo sapiens cDNA
7673	25851	34217	0.85	2.0E-55	AW501988.1	EST_HUMAN	UI-HF-BND-als-4-06-0-ULI NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8285	22342	35802	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3134463 3'
8285	22342	35893	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3134463 3'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9381	22436		4.33	2.0E-55	A002836.1	EST_HUMAN	arr68h05.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains TTR.D2 THR repetitive element;
9442	22510		0.67	2.0E-55	BE007969.1	EST_HUMAN	QV0-BN0147-280400-213-g06 BN0147 Homo sapiens cDNA
11192	24261	37897	2.33	2.0E-55	AU118944.1	EST_HUMAN	AU118944 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
13177	16198	29222	1.34	2.0E-55	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBES3A) mRNA
89	13334	28361	1.82	1.0E-55	4505060	NT	Homo sapiens mannose-8-phosphate receptor (cation dependant) (M8PR) mRNA
194	13417	26446	40.5	1.0E-55	U08823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
598	13779	26786	1.88	1.0E-55	A028718.1	EST_HUMAN	ov85g09.X1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1644160 3'
1173	14336	27392	3.82	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2006	15146	28251	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2006	15146	28262	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2401	15332		4.85	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2415	15397	28673	1.44	1.0E-55	AF000980.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2586	16711	28829	19.88	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2620	15743	28857	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2620	16743	28868	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2677	15797	28914	3.37	1.0E-55	L64057.1	NT	Homo sapiens CLP mRNA, partial cds
2850	15864	29073	1.22	1.0E-55	AB033046.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3495	16662	29674	1.16	1.0E-55	W28189.1	EST_HUMAN	43-c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4097	17282	30253	4.28	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4409	17551	30536	1.1	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4853	17886		0.94	1.0E-55	N77261.1	EST_HUMAN	yv4403.11 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:245620 5'
4949	18079	31054	1.15	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
4949	18079	31055	1.15	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
5614	18808	31876	0.65	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6401	19570	32832	7.26	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6401	19570	32833	7.26	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8178	21280	34762	1.7	1.0E-55	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapeym-110) (DLG2), mRNA
8178	21280	34763	1.7	1.0E-55	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8266	21348	34853	0.49	1.0E-55	11421949	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
8273	21365	34872	0.93	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8273	21365	34873	0.93	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11152	24223	37851	2.41	1.0E-56	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11152	24223	37852	2.41	1.0E-56	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11733	23919	37544	1.86	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11755	23941	37567	1.34	1.0E-56	T10045.1	EST_HUMAN	seq1676 b4-HB3MA Co8-HAP-F1 Homo sapiens cDNA clone b4-HB3MA-COT8-HAP-F161 5' similar to similar to Chinese Hamster DHFR-overexpressed protein mRNA
11789	24779	38478	2.67	1.0E-55	8822743	NT	Homo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA
11878	24864	38560	1.78	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7522	20585	34070	1.85	9.0E-56	BE378074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608552 5'
11545	24601	38277	1.34	8.0E-56	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2783	15909	23017	7.08	7.0E-56	H18934.1	EST_HUMAN	yn62g03.1 Scores adult brain N254HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THIR repetitive element ;
7818	20873	34371	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-019-507 CT0252 Homo sapiens cDNA
7818	20873	34372	1.98	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-019-507 CT0252 Homo sapiens cDNA
1727	14877	27968	2.7	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-401 BN0053 Homo sapiens cDNA
9362	22437	35965	0.71	5.0E-56	AW015507.1	EST_HUMAN	UIH-B10p-eau-e-05-Q-J1a1 NCJ_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10589	23634	31550	1.35	5.0E-56	W28189.1	EST_HUMAN	43c-5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12513	28137	26268	2.47	5.0E-56	H55098.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_56 5'
28	13266	26268	8.94	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
28	13266	26269	8.94	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2773	15888	28908	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	15888	28909	3.61	4.0E-56	4507728	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2873	13732	26756	9.22	4.0E-56	AF003528.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19596	32915	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19596	32916	4.94	4.0E-56	AF217508.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10724	23757	37384	1.89	4.0E-56	AF043949.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11163	24234	37863	7.73	4.0E-56	AI498066.1	EST_HUMAN	hm65g12.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
11163	24234	37864	7.73	4.0E-56	AI498066.1	EST_HUMAN	hm65g12.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
1372	14527	27801	2.69	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1804	14953	28047	1.84	3.0E-56	6912743	NT	Homo sapiens 5'-3' acetyltransferase 2 (XRN2), mRNA
2217	15351	28482	1.6	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3195	16370	29378	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3195	16370	29377	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3939	17098		2.81	3.0E-56	AF055068.1	NT	Homo sapiens MHC class I region

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4507	17849	30834	0.87	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
4544	17682	30864	4.42	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4686	17830	30816	2.4	3.0E-56	5902085	NT	Homo sapiens superfamily viral-like activity 2 (S. cerevisiae homolog)-like (SKIVL), mRNA
5801	18891	32283	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteonecin, cncv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA
5801	18891	32284	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteonecin, cncv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA
7014	20150	33571	5.5	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7476	20561	34023	2.07	3.0E-56	4504870	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
7476	20561	34024	2.07	3.0E-56	4504870	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
8016	22086	35835	6.11	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10018	23058	36852	0.9	3.0E-56	D63478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10698	23731	37336	1.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10880	24059	37883	2.62	3.0E-56	AB042558.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
11594	24647	38330	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11594	24647	38331	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
12377	25268	32075	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12377	25268	32076	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
637	13730		11.95	2.0E-56	AA198818.1	EST_HUMAN	z652a08.s1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645206 3'
761	18021	26876	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-F10 BT0310 Homo sapiens cDNA
761	18021	26876	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
3053	16229	28249	0.94	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3391	16561		0.84	2.0E-56	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3824	18788	28805	1.26	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCF-G10 5'
7239	20323	33767	1.39	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA
1003	14174		3.01	1.0E-56	AF190830.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3765	18826	28828	1.84	1.0E-56	AW588833.1	EST_HUMAN	hg23G11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2846452 3'
3765	18826	28829	1.84	1.0E-56	AW588833.1	EST_HUMAN	hg23G11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2846452 3'
5145	18268	31238	1.42	1.0E-56	AB05162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
10161	23188		0.89	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10254	23289	36886	1.52	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220689-001-E02 CT0163 Homo sapiens cDNA
642	18927		1.39	9.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070300-162-H03 OT0033 Homo sapiens cDNA
11494	24552	38227	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11494	24552	38228	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11811	24801	38500	2.2	8.0E-57	AB020881.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
14	13252	28252	1.02	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
308	13524	28558	2.93	8.0E-57	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
907	14082	27147	7.49	8.0E-57	AW264939.1	EST_HUMAN	3x05d10.x1 NCI CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 5' similar to gb:U05875
1859	15005	28112	1.45	8.0E-57	AA486109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5355	28034	31879	1.92	8.0E-57	11418185	NT	2x51b12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
6529	19893	33066	0.81	8.0E-57	AB020705.1	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), mRNA
6593	19753	33138	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0888 protein, partial cds
6593	19753	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
7607	20877	34152	0.62	8.0E-57	7682263	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7627	20977	34486	1.54	8.0E-57	AB020644.1	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7627	20977	34487	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11768	13252	28252	3.51	8.0E-57	8923349	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
12041	25022	38726	1.74	8.0E-57	11433356	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12102	25082	38789	1.53	8.0E-57	11431260	NT	Homo sapiens ninnin (LOC51189), mRNA
12791	25528	32007	1.87	8.0E-57	11545732	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12808	25528	32007	1.94	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1246	14405	27467	0.88	7.0E-57	AJ003100.1	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2698	15817	28932	0.97	7.0E-57	7657592	NT	Homo sapiens GYS2 gene, exon 14
2698	15817	28933	0.97	7.0E-57	7657592	NT	Homo sapiens sng GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3344	16517	29532	0.81	7.0E-57	6005978	NT	Homo sapiens sng GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3982	17139	30143	3.14	7.0E-57	AF012872.1	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3982	17139	30144	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
13185	26071		3.99	5.0E-57	AJ271735.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
3949	17009	30010	8.03	4.0E-57	AB026998.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2
827	14005	27062	0.64	3.0E-57	4507798	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4 genes, complete cds)
1302	14516		12.47	3.0E-57	AA230279.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
2484	15391	28718	1.12	3.0E-57	AA348335.1	EST_HUMAN	nc1307.st NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:4008037 similar to SW_RS10_HUMAN
2708	15883	28992	1.03	3.0E-57	BE876822.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10. ; EST64770 Hippocampus II Homo sapiens cDNA 5' and 783b10.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H9C.2 CE20263 ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2768	15883	28093	1.03	3.0E-57	BE076822.1	EST_HUMAN	733b10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y4749C.2
3652	16816	28827	1	3.0E-57	AF232708.1	NT	CE20283 ; Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
3788	16849		51.29	3.0E-57	AW833684.1	EST_HUMAN	RC3-CT0254-110300-027-410 CT0254 Homo sapiens cDNA
6183	18329	32675	1.25	3.0E-57	11225808	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6251	18425	32771	3.25	3.0E-57	BE798837.1	EST_HUMAN	601588886F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8338	21419	34945	3.92	3.0E-57	W28130.1	EST_HUMAN	4218 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8363	21444	34966	1.89	3.0E-57	11545788	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8363	21444	34967	1.99	3.0E-57	11945798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8476	21557	35090	0.78	3.0E-57	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8624	21704	35240	0.62	3.0E-57	J05282.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
8050	22139	35882	5.14	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001810 5'
9451	22567	36132	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
9451	22567	36133	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
11148	24220	37847	2.34	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	26167	31654	0.37	3.0E-57	W23871.1	EST_HUMAN	zb45d11.1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12882	25640	31984	1.17	3.0E-57	AJ003349.1	EST_HUMAN	AJ003349 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp10-1L1
1630	14683	27762	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1630	14683	27763	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2760	15908	28014	5.5	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares_peritubular_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains ALU repetitive element; contains element MER22 repetitive element ;
3525	16890		1.4	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3641	16805	28818	0.72	2.0E-57	R07702.1	EST_HUMAN	ye88h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3641	16805	28819	0.72	2.0E-57	R07702.1	EST_HUMAN	ye88h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4304	17447	30433	0.71	2.0E-57	AA018289.1	EST_HUMAN	ze40c08.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361460 5'
4304	17447	30434	0.71	2.0E-57	AA018289.1	EST_HUMAN	ze40c08.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361460 5'
4632	17768	30749	7.42	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C008
6785	18977		1.48	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
6158	18334		31.41	2.0E-57	BF115288.1	EST_HUMAN	7n80f04.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3870966 3' similar to contains TAR1.1f
6288	19461	32813	6.34	2.0E-57	11431281	NT	MER22 repetitive element ;
8832	21911	35449	1.03	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
10051	23089	36681	1.06	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
						NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4